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******	(M)	*****

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Sep 2 11:18:27 1999; MasPar time 8.07 Seconds 60.852 Million cell updates/sec

ular output not generated.

Description:
Perfect Score:
Sequence: >US-08-599-226-3 (1-9) from US08599226.pep 66 1 QRYNRAPYX 9

Scoring table: PAM 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Stàtistics: Mean 22.838; Variance 29.153; scale 0.783

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

ult No.	Score	% Query Match	Length DB	ij	Description	Pred. No.
1	57	86.4	560	044626	K11D12.1 PROTEIN.	3.24e-01
N	54	81.8			PRTC.	1.40e+00
ω	54	81.8			20S PROTEASOME SUBUNIT	1.40e+00
4	54	81.8		002441	GDP-DISSOCIATION INHIB	1.40e+00
ر.	54	81.8				1.40e+00
6	53	80.3		2 Q55956	ABC TRANSPORTER.	2.27e+00
7	52	78.8			R11.2 PROTEIN.	3.64e+00
8	52	78.8		P92024	MEX-1.	3.64e+00
9	52	78.8	509 5	Q21017	COSMID F58H12.	3.64e+00
10	51	77.3			SIMILARITY WITH HEAD C	5.81e+00
11	50	75.8	178 4		CD89_L10.	9.23e+00
12	50	75.8	201 /	Q99935	BASIC PROLINE-RICH PRO	9.23e+00
13	50		332 10	082438	ANTIFREEZE PROTEIN.	9.23e+00
14	50	75.8	450	050511	ZINC PROTEASE.	9.23e+00
15	50	75.8	521	2 044677	NEUTRAL PROTEASE.	9.23e+00
16	50	75.8		036979	POLYPROTEIN.	9.23e+00
17	49	74.2	641	018586	COSMID C43H6.	1.46e+01
18	48	72.7	43 10	049246	REVERSE TRANSCRIPTASE	2.28e+01
19	48	72.7	44 10	049247	REVERSE TRANSCRIPTASE	2.28e+01
20	48	72.7	192 !	5 Q1900B	COSMID D2096.	2.28e+01

Query Match

86.48;

Score 57;

DB ű

Length 560;

3.55e+01	DROGENASE	052485	1312 2		47
	HYPOTHETICAL 82.1 KD P	023337		71.2	47
3.55e+01		Q60447		71.2	47
3.55e+01	F10D2.11 PROTEIN.	016922		71.2	47
3.55e+01	HYPOTHETICAL 55.3 KD P	055733	ш	71.2	47
3.55e+01	GDP DISSOCIATION INHIB	043928		71.2	47
3.55e+01	GUANOSINE DIPHOSPHATE	Q61598	445 11	71.2	47
	RABGDI PROTEIN.	Q21449		71.2	47
3.55e+01	HYPOTHETICAL 47.6 KD P	Q10929		71.2	47
	UNC-101 PROTEIN.	002282		71.2	47
3.55e+01	HYPOTHETICAL 41.6 KD P	P74732	355 2	71.2	47
3.55e+01	FMRFAMIDE (FRAGMENT).	Q24955		71.2	47
2.28e+01	HEMOCYANIN G-TYPE SUBU	061363		72.7	48
2.28e+01	MYELOBLAST KIAA0230 (F	Q92626		72.7	48
•	DENSIN-180.	P70587	1495 11	72.7	48
	HYPOTHETICAL 117.2 KD	P72637	1032 2	72.7	48
	HYPOTHETICAL 77.8 KD P	074504		72.7	48
2.28e+01	FORKHEAD ACTIVIN SIGNA	P70056	534 13	72.7	48
2.28e+01	ATP-DEPENDENT PROTEINA	082974		72.7	48
	FORK HEAD PROTEIN.	Q91904		72.7	48
2.28e+01	FORK HEAD PROTEIN.	Q91905		72.7	48
2.28e+01	ORF40X1 PROTEIN.	034232		72.7	48
2.28e+01	ORF139-17 PROTEIN.	087136		72.7	48
2.28e+01	TRANSPOSASE HOMOLOG.	050244	307 2	72.7	48
7.28e+01	HYPOTHETICAL 25.6 KD P	0/4961		12.1	4

# ALIGNMENTS

SEQ	PRO ZIN	SUB	SEQ	STR SUB	NAT [2]	"2.	SMA	LIG	GARDN	BON	WIL	SEQ	RHA	CAE	<u> </u>	01-	01-	SULT 1 044626
FOIENCE SEO AA.	EMBL; AF03904/; GZ/36445; PROSITE; PS00028; ZINC_FI ZINC-FINGER: METAL-BINDIN	WATERSTON R.; SUBMITTED (DE	SEQUENCE FROM N.A. STRAIN=BRISTOL N2;	STRAIN-BRISTOL N2; HENKHAUS J., WOHLI SUBMITTED (JAN-199	NATURE 368:3 [2] SEQUENCE FRO	WATSON A., WEINSTOCK L., WILKINSO "2.2 Mb of contiguous nucleotide Glegons":		LIGHTNING J.	ER A.	· 4 ·	MEDLINE; 941	UENCE AIN≃BI	BDITINA;	CAENORHABDITIS ELEGANS. EUKARYOTA: METAZOA: NEMATODA:	K11D12.1 PRC K11D12.1.	01-NOV-1998	01-JUN-1998	626
	METAL-B	R.; (DEC-1997)	FROM N.A. RISTOL N2;	OL N2; WOHLDMANN P., AN-1998) TO EM	368:32-38(1994). CE FROM N.A.	ontiguou	SMITH A.,	PERCY C.	KERSHAW J. K		94150718.	FROM N.A.	RHABDITO	IS ELEGANS	PROTEIN.	(TREMBLREL.	(TREMBLREL.	PRELIMINARY;
1	NC_FINGER	TO EMBL/		NN P., GI	<del>.</del>	L., WILK nucleot	SONNHAMMER	RIFKEN I			R . ANDE		IDEA; RHA	NS.		, 80 90	96,	ARY;
200000000000000000000000000000000000000	EMBL; AF039047; G27/36445; PROSITE; PSO0028; ZINC_FINGER_C2H2; 1. ZINC-FINGER: METAL-BINDING: DNA-BINDING	_EMBL/GENBANK/DDBJ		ISTOL N2; J., WOHLDMANN P., GILLAM B.; (JAN-1998) TO EMBL/GENBANK/DDBJ		weinstock L., Wilkinson-Sproat J., Wohldman P.; contiguous nucleotide sequence from chromosome	DNNHAMMER E., STADEN R., SU K., VAUDIN M., VAUGHAN K.,			BURTON J., CONNELL M., COPSEY T.,	ANDERSON K . BAYNES		RHABDITINA; RHABDITOIDEA; RHABDITIDAE;	SECERNENTEA:		LAST ANNOT	н	PRT; 5
	ភ	DBJ DATA		DBJ DATA		nce from	E., STADEN R., SULSTON J., IN M., VAUGHAN K., WATERSTO	A., MORTIMORE B., O'CALLAGHAN M., ROODRA A SAIINDERS D SHOWNKEEN	HILLIER L., JIER M., JOHN	PSEY T.,	BAYNES C.		PELC			ANNOTATION UPDATE		560 AA.
		BANKS.		BANKS.		from chromosome	, SULSTON	B., O'C	JIER M., JOI	PER	BERKS			RHABDITIA: I		UPDATE)		
						P.; me III of	WATERSTON R.	SHOWNK	JOHNSTON		<b>X</b>		CAENORHABDITIS	RHABDITIDA				
						f C.		NIC N	L.,	ON A.,			TIS.					

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Matches
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Matches
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                                                                                                                                                                                            042265;
042265;
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Q27562
Q27562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00388; PROTEASOME_A; 1.
PEAM; PE00227; proteasome 1
PROTEASOME
                                                                                                                                              01-JAN-1998 (TREMBLREL. 05, 01-AUG-1998 (TREMBLREL. 07, 01-NOV-1998 (TREMBLREL. 08, 20S PROTEASOME SUBUNIT C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SHAULENT G., ESCALANTE R., LOOMIS W.F.;
SUBMITTED (JUN-1996) TO EMBL/GENBAUK/DDBJ DATA BANKS.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S25A; ALSO KNOWN AS THE PROTEASOME A-TYPE FAMILY.

-!- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRTC.
                                  SEQUENCE FROM N.A.
SINGH I., WAGNER B.J.;
SUBMITTED (MAY-1998) TO EL
EMBL; AF027978; G3136063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). EUKARYOTA; DICTYOSTELIUA; DICTYOSTELIUM.
                                                                                                            GALLUS GALLUS
EUKARYOTA; MET
                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00227; proteasome; 1 PROTEASOME; HYDROLASE; PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷
                     PFAM; PF00227; proteasome;
                                                                                                NEOGNATHAE;
                                                                                                                                                                                                                                                                                 121 QRYGRRPY
            ROTEASOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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                                                                                                                                                                                                                                                                                                          Local Similarity
les 6; Conse
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                                                                                                                                                                                                                                                           1 QRYNRAPY
                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL PROTEOLYTIC PATHWAY.

SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL SUBUNITS WHICH FORM A HIGHLY ONDERED RING-SHAPED STRUCTURE.

SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND ALSO IN THE NUCLEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH.
THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY.
THE COMPONENT C3 MAY HAVE A POTENTIAL REGULATORY EFFECT ON ANOTHER COMPONENT(S) OF THE PROTEASOME COMPLEX THROUGH TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRYNRAPY
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                                                                                                            LUS (CHICKEN).
METAZOA; CHORDATA;
260 AA;
                                                                                                                                                                                                                                                                                                                                                           248 AA;
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                                                                                                GALLIFORMES;
                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Conservative
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                                                                                                                                                                                                                                                                                   128
                                                                                                                                                                                                                                                                                                                      81.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                         27988 MW;
28925
                                                TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                     PROTEASE.
                                                                                               ATA; VERTEBRATA; ARCHOSAURIA; AVES; PHASIANIDAE; PHASIANIDAE; GALLUS.
 W.
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Pred.
0; M
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2; M
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LAST SEQUENCE UPDATE)
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EF38499F CRC32;
                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                       54;
No.
                                                                                                                                                                                                                                                                                                       Db ;
. 1.40e+00;
-hag 2;
                                                                                                                                                                                                            260
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                                                DATA
                                                                                                                                                                                                                                                                                                                                 Length 248;
                                                BANKS
                                                                                                                                                                                                                                                                                                            Indels
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Best Local S
Matches
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Best Local S
Matches
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017517
017517; PRELIMINARY;
01-JAN-1998 (TREMBLREL 05, CF
01-JAN-1998 (TREMBLREL 05, L
01-NOV-1998 (TREMBLREL 08, I
                                                                                                                                                                                                                                                                              BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATERSTON R., WATESON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; PARSON B., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; PARSON B., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1997
01-JUL-1997
01-NOV-1998
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ZC1
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MUELLER W.E.G.;
AQUATIC TOXICOL. 37:157-168(1997).
EMBL; X94983; E218570; -.
PFAM; PF00996; GDI; 1.
SEQUENCE 448 AA; 50215 MW; 848
                                                      STRAIN-BRISTOL N2;
BRADSHAW H., DEVLIN
SUBMITTED (JUL-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
MEDLINE; 94150718.
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EUKARYOTA; METAZOA; PORIFERA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDP-DISSOCIATION INHIBITOR.
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   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%;
ilarity 62.5%;
Conservative
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                                                            ) K
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75.0%;
                                                            EMBL/GENBANK/DDBJ DATA BANKS
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Pred. No. 1.40e+00;
2; Mismatches 1
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Pred.
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1. No. 1.40e+00;
Mismatches 2;
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DDERINAE; CAENORHABDITIS.
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RESULT 6
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AC Q55956;
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01-NOV-1996
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01-AUG-1998
01-JAN-1999
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062346;
                                                                                                                                                                                                                                                                                                                                             KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAI MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YINBATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUGIURA M., TABATA S.;
Suguence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. I. sequence features in the 1Mb region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             877 QRYNRAP
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WATERSTON R.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AF014939; G2275629; -.
SEQUENCE 1277 AA; 146496 MW; 8A6DB899 CRC32;
                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABC TRANSPORTER. SYNECHOCYSTIS SE
                      CAENORHABDITIS ELEGANS. EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                PFAM; PF00005; ABC_tran; 1. PFAM; PF00498; FHA; 2.
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MEDLINE; 96127529.
 RHABDITINA; [1]
                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Local Similarity 100.0%;
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CYANOBACTERIA; C
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8 (TREMBLREL.
9 (TREMBLREL.
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(TREMBLREL.
             RHABDITOIDEA;
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87656 MW;
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CHROOCOCCALES;
             RHABDITIDAE;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                        Score 53; DB 2;
Pred. No. 2.27e-
3; Mismatches
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Pred. No. 1.40e+00;
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          SECERNENTEA; RHABDITIA; RHABDITIDA;
BDITIDAE; PELODERINAE; CAENORHABDITI
                                                                                                                PRT;
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                                                                                                                                                                                                                  53; DB 2; I
No. 2.27e+00;
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           CAENORHABDITIS
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                                                                                                                                                                                                                                                                                                                                                         M., YASUDA M.,
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RESULT 9
ID Q21017;
AC Q21017;
DT 01-NOV-1996 (TREMBLREL.
DT 01-NOV-1996 (TREMBLREL.
DT 01-NOV-1998 (TREMBLREL.
DT 01-NOV-1998 (TREMBLREL.
DE COSMID F58H12.
GN F58H12.1
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMAYOTA;
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ID P92024
AC P92024;
DT 01-MAY-1997
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GUEDES S.,
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DURBLIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER L., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., RODERA A., SAUNDERS D., SHOWNKEEN
RALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED
                                                                                                                                                                                                                                                       "The C. elegans MEX-1 protein is a P granule component."; DEVELOPMENT 124:731-739(1997). EMBL; U81043; G1899062; -. PFAM; PF00642; zf-CCCH; 2.
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EUKARYOTA; METAZOA; NEMATODA;
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EMBL; 281577; E1348694;
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"2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCMURRAY A.;
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     MEX-1
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6; Conse
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                                                                                                 PRELIMINARY;
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larity 62.5%;
Conservative
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Pred. No. 3.64e+00;
1; Mismatches 1
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Pred. No. 3.
 SECERNENTEA; RHABDITIA; RHABDITIDA;
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                                                                                                                                                                                                                                             716506D2 CRC32;
                                                                                                                                                                                              Mismatches
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                                                                                                 509
                                                                                                                                                                                                          DB 5; L
3.64e+00;
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                                                                                                                                                                                                                                                                                                        germline blastomeres
                                                                                                                                                                                                                    Length 494;
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Matches
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Best Local
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CD89_L10.
HOMO SAPIENS (HUMAN).
                                            JLT 11
Q92592
Q92592;
Q92592;
01-FEB-1997
01-FEB-1997
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                    048279 PRELIMINARY; PRT; 170 AA. 048279; 01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION PROTEIN. SIMILARITY WITH HEAD COMPLETION/STABILIZATION PROTEIN.
                                                                                                                                                                                                                                            PONTAROLLO R.A.;
THESIS (1995), V. I. D. O., UNIVERSITY OF
EMBL; U28154; G915368; -.
SEQUENCE 170 AA; 19923 MW; 91428D5E CH
                                                                                                                                                                                                                                                                                                                                                HAEMOPHILUS SOMNUS.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (NOV-1995) TO EMBL; U40416; G1065490; SEQUENCE 509 AA; 5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WATSON A., WEINSTOCK L., WILKINSC "2.2 Mb of contiguous nucleotide elegans.";
                                                                                                                                                                                                                                                                                                STRAIN-HS25
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 368:32-38(1994).
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7 (TREMBLREL.
9 (TREMBLREL.
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71.4%;
       CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55953 MW;
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                                                                                                                                                                                            Score 51; D
Pred. No. 5.
1; Mismatc
                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred.
1; M
         VERTEBRATA;
                                                                                                                                                                                                                                               91428D5E CRC32
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NO.
                                                                                             178
                                                                                                                                                                                                         DB 2; L
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         MAMMALIA;
                                                                                                                                                                                                                                                                       SASKATCHEWAN
                                                                                                                                                                                                                     Length 170;
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         EUTHERIA;
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         PRIMATES;
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RESULT

AC OSC

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DT O12

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DT O13

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JAC Q9
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Best Local
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Best Local
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(Q99935; PRELIMINARY;
(Q99935; CTREMBLREL 03, C
01-MAY-1997 (TREMBLREL 03, C
01-MAY-1997 (TREMBLREL 08, L
01-NOV-1998 (TREMBLREL 08, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Alternatively spliced f
with IgA nephropathy.";
submirred (SEP-1996) TO
EMBL; D87861; D1014171;
SEQUENCE 178 AA; 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                JLT 13

082438;

01-NOV-1998

01-NOV-1998

01-NOV-1998

ANTIFREEZE PI
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CURR. EYE RES. 15:37-386(1996
EMBL; S83198; G1836022; -.
SEQUENCE 201 AA; 22870 MW;
                                                                                                                                                       STRAIN-CV. AUTUMN KING MEDLINE; 98429644. WORRALL D., ELIAS L.,
                                                                                                                                                                                                                                                                                                                              DAUCUS CAROTA (CARROT).
EUKARYOTA; VIRIDIPLANTAE; STREI
EUPHYLLOPHYTES; SPERMATOPHYTA;
                                                  LILLEORD P., TELFORD J., HOLT
"A carrot leucine-rich repeat
recrystallization.";
SCIENCE 282:115-117(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DICKINSON D.P., THIESSE M.; "CDNA cloning of an abundan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 96309097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC PROLINE-RICH
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[1]
  SEQUENCE
                              EMBL;
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                                                                                                                                                                                                                                                                                                    ASTERIDAE;
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                              AF055480; G3702803;
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                                                                                                                                                                                                                   AUTUMN KING;
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llarity 62.5%;
Conservative
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llarity 71.4%;
Conservative
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                                                                                                                                       ASHFORD
J., HOLT
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d forms
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  WW;
                                                                                                                                                                                                                                                                                                 STREPTOPHYTA; EMBRY
HYTA; MAGNOLIOPHYTA;
ACEAE; DAUCUS.
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Pred. No. 9.
2; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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2; M
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I C., BOWLES D.
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  67194791 CRC32;
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                                                                                                                                                          SMALLWOOD M.,
                                                                                                                                                                                                                   ROOT;
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9.23e+00;
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Best Local Similarity
Matches 4; Conser
Query Match
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STRAIN-A3(2);
PARKHILL J., BARRELL E
SUBMITTED (NOV-1997) T
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050511;
                                                                                                                                                                                                                                                    Q44677;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NEUTRAL PROTEASE.
BACILLUS AMYLOLIQUEFACIENS.
BACILLUS AMYLOLIQUEFACIENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2);
MEDLINE; 97000351.
REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map
"A set of ordered cosmids and a detailed genetic and physical map
"A set of ordered cosmids and a detailed genetic and physical map
"B set of ordered cosmids and a detailed genetic and physical map
"B set of ordered cosmids and a detailed genetic and physical map
"B set of ordered cosmids and a detailed genetic and physical map
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01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
2INC PROTEASE.
2COBLO.04.
3COBLO.04.
STREPTOMYCES COELICOLOR.
BACTIRLA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
BACTIRLA; STREPTOMYCINEAE; STREPTOMYCES.
                                         J. BIOTECHNOL. 2:75-85(1985).

EMBL; M36723; G143353; -

PFAM; PF00099; zn-protease; 1

PROTEASE

SEQUENCE 521 AA; 56725 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            Q44677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLIVER K., HARRIS D.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-A3(2);
                                                                                                                                                                          SEQUENCE FROM N.A.
SHIMADA H., HONJO M., MITA I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                            FURUTANI Y.;
                                                                                                                                                                                                                                                  BACILLUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 QRFDRTAY 318
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llarity 50.0%;
Conservative
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                                                                                     zn-protease; 1.
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62.5%;
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                                           56725 MW;
  75.8%;
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TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 2; I
Pred. No. 9.23e+00;
1; Mismatches 2
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Pred. No. 9.23e+00;
4; Mismatches 0;
  Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3E30B71A CRC32;
                                           64AFFE5F CRC32;
                                                                                                                                                                                 NAKAYAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450 AA
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DB 2;
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Length 521;
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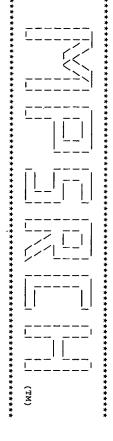
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Best Local Similarity 62.5%; Pred. No. 9.23e+00; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps

Db 308 QKYNRNSY 315

| | | | | | | | |
QY 1 QRYNRAPY 8
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Search completed: Thu Sep 2 11:18:44 1999 Job time: 17 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 11:21:51 1999; MasPar time 4.46 Seconds 146.856 Million cell updates/sec

Sular output not generated.

Description: Perfect Score: >US-08-599-226.pep (1-12) from US08599226.pep 66 1 VSYLSTASSLDX 12

Sequence:

Scoring table:

PAM 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 23.196; Variance 28.631; scale 0.810

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

No.	Score	Query	Length	DB	Ħ	Description	Pred. No.
ב	55	83.3	649	ω	060167	PROTEIN COMPLEX ASSEMB	8.09e-01
2	51	77.3	236	ω	Q12282	CHROMOSOME XV READING	5.65e+00
ω	51	77.3	3623	11	070244	INTRINSIC FACTOR-B12 R	5.65e+00
4	50	75.8	293	2	051095	CONSERVED HYPOTHETICAL	9.06e+00
ۍ	50	75.8	705	N	P94888	CADMIUM RESISTANCE PRO	9.06e+00
o	49	74.2	599	ν	084716	PHOSPHOENOLPYRUVATE CA	1.44e+01
7	48	72.7	292	14	055748	PUTATIVE RIBONUCLEASE.	2.28e+01
8	48	72.7	467	4	043298	KIAA0414.	2.28e+01
9	48	72.7	832	4	Q92831	P/CAF.	2.28e+01
10	48	72.7	1245	v	016568	F40E12.2 PROTEIN (FRAG	2.28e+01
11	47	71.2	127	14	011696	NUCLEOPROTEIN (FRAGMEN	3.58e+01
12	47	71.2	149	11	Q61836	MYELIN BASIC PROTEIN (	3.58e+01
13	47	71.2	195	11	Q01585	MYELIN BASIC PROTEIN (	3.58e+01
14	47	71.2	197	4	Q15339	GOLLI-MBP.	3.58e+01
15	47	71.2	239	N	Q00510	SRMX PROTEIN.	3.58e+01
16	47	71.2	250	11	Q03139	MYELIN BASIC PROTEIN (	3.58e+01
17	47	71.2	255	10	023112	AP2 DOMAIN CONTAINING	3.58e+01
18	47	71.2	303	14	Q84594	SIMILAR TO PBCV-1 SERI	3.58e+01
19	47	71.2	304	4	Q15340	GOLLI-MBP.	3.58e+01
20	47	71.2	458	4	060326	KIAA0582 PROTEIN (FRAG	3.58e+01

4 4 5	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
45	45	45	45	45	45	45	45	45	45	45	45	45	45	46	46	46	46	46	46	46	47	47	47
68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	69.7			69.7	69.7	69.7	69.7		71.2	71.2
1369	631	619	809	546	471	448	384	370	276	261	164	131	121	2910	1022	503	500	296	258	133	1128	1128	959
2 13	2	4	10	2	10	σ	2	10	œ	ш	ъ	14	14	5	σ	G	N	14	5	N	Ь	ш	5
050417 P79950	086216	Q13042	P92973	069236	023552	077045	Q11197	065492	Q33658	059473	Q23378	090638	090626	Q26008	Q28628	Q26594	025869	Q69118	Q19850	084670	051999	052009	018359
MULTI-FUNCTIONAL ENZYM TYROSINE KINASE RECEPT		CDC16HS.	CCA1.	MERCURIC REDUCTASE.	HYPOTHETICAL 52.8 KD P	NWEG PRECURSOR (EC 3.2	HYPOTHETICAL 41.9 KD P	42	ATP SYNTHASE A CHAIN (	261AA LONG HYPOTHETICA	COSMID ZC64.	GLYCOPROTEIN GJ.	GLYCOPROTEIN GJ.	RNA POLYMERASE I.	A-KINASE ANCHORING PRO	AMINO ACID PERMEASE.	ANTHRANILATE SYNTHASE	HYPOTHETICAL PROTEIN (	COSMID F28B12.	HYPOTHETICAL 14.7 KD P	REPI PROTEIN.	REPJ PROTEIN.	PUTATIVE KRUEPPEL TARG
8.64e+01 8.64e+01		8.64e+01	8.64e+0	8.64e+01	8.64e+01		8.64e+01	٠	•	8.64e+01			8.64e+01	5.58e+01				5.58e+01					3.58e+01

R R R R R	\$666644444	RESULT	Оў	M B Q	SOREARS	200000	RESULT ID O AC O DT 0 DT 0 DT 0
SEQUENCE FROM N.A.  BOYER J., FAIRHEAD C., GAILLON L., GALISSON F., MICHAUX G., THIERRY A., DUJON B.; SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.	01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) CHROMOSOME XV READING FRAME ORF YOR214C. SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES; SACCHAROMYCETACEAE; SACCHAROMYCES.	LT 2 012282 PRELIMINARY; PRT; 236 AA.	233 INYLSTARSLE 243 ::       : 1 VSYLSTASSLD 11	Query Match 83.3%; Score 55; DB 3; Length 649; Best Local Similarity 63.6%; Pred. No. 8.09e-01; Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	SEQUENCE FROM N.A. STRAIN-972H-; BECK A., REINHARDT R., WOOD V., RAJANDREAM M.A., BARRELL B.G.; SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AL023594; E1293401; SEQUENCE 649 AA; 72985 MW; 9C207DB2 CRC32;	SPBC1978.03C. SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES; SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE; SCHIZOSACCHAROMYCES.	OF THE TOTAL OF THE TABLE OF TH

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RESULT OF THE RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDITURE: 98148073

A MOESTRUP S.K., KOZYRAKI R., KRISTIANSEN M., KAYSEN J.H.,

A RASMUSSEN H.H., BRAULT D., PONTILLON F., GODA F.O., CHRISTENSEN E.I.,

A HAMMOND T.G., VERROUST P.J.;

"The intrinsic factor vitamin Bl2 receptor and target of teratogenic

antibodies is a megalin-binding peripheral membrane protein with

thomology to developmental proteins.";

homology to developmental proteins.";

J. BIOL. CHEM. 273:5235-5242(1998).

REMBL; AFO22247; G3834380; -.

RPROSITE; PS001010; ASX.HYDROXYL; 3.

RPROSITE; PS001187; EGF_CA; 4.

RPROSITE; PS01187; EGF_CA; 4.

REMBL; GLYCOPROTEIN; EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Consei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE: .....
STRAIN-FY1679;
STRAIN-FY1679;
GALISSON F., DUJON B.;
GALISSON F., DUJON B.;
GENBL; Z75122; E252081; -.
EMBL; Z75122; E252081; -.
EMBL; X92441; G1050766; -.
EMBL; X92441; G1050766; -.
                                                                                                                                                               O51095 PRELIMINARY;
O51095;
01-JUN-1998 (TREMBLREL. 0
01-JUN-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O70244

PRELIMATION
O70244;
O70244;
O70244;
O1-2046-1998 (TREMBLREL. 07, CREATED)
O1-JAN-1999 (TREMBLREL. 09, LAST SEQUENCE UPDATE)
O1-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
O1-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
SEQUENCE
                                                                                                                                                  CONSERVED HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED
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SEQUENCE FROM N.A.
     SEQUENCE FROM N.A. STRAIN-ATCC 35210
       STRAIN ATCC
                                                                         BORRELIA BURGDORFERI (LYME BACTERIA; SPIROCHAETALES; S
                                                                                                                            8900EB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                          697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175
                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 77.3%;
Local Similarity 54.5%;
les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H
                                                                                                                                                                                                                                                                                                                                                                    VSYLSTASSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                     ITYLTTQSDLD 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISYLSSTISL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 36
3623 AA;
                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.3%;
larity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3623
A; 398981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO EMBL/GENBANK/DDBJ
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                                                                                                                                             06, CREA
06, LASI
08, LASI
PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GENBANK/DDBJ DATA BANKS
                                                                         SPIROCHAETACEAE; BOR
                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 3; L
Pred. No. 5.65e+00;
4; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 11; L
Pred. No. 5.65e+00;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
INTRINSIC FACTOR-B12 RECEPTOR.
MW; ADF804DC CRC32;
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; E; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9759C243
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                                                                           BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3623;
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RESULT AC PROCESSION OF PROCES
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Best Local S
Matches
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Best Local S
Matches
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PFAM; PF00122; E1-E2_ATPASE; 1.
PFAM; PF00403; HMA; 1.
PFAM; PF00403; HMA; 3.
PLASMID; HYDROLASE; TRANSMEMBRANE
MOD_RES 398 990
SEQUENCE 705 AA; 76466 MW; 66
                                                                                                                                                                                                                               LT 6
084716
084716;
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01-MAY-1997
01-NOV-1998
                                                                                                                                            01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOSPHOENOLPYRUVATE CARBOXYKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATURE 390:580-586(1997).
EMBL; AE001120; G2687956; -.
TIGR; BB0068; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98065943.

FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A., LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M LATHIGRA R., WHITE O., FLEISCHMANN R.D., RICHARDSON D., PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J., UTTERBACK T., WAITHEY L., MCDONALD L., ARTIACH P., BOWMAN C., GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B., SMITH H.O., VENTER J.C.;
    STRAIN-D/UW-3/CX;
STEPHENS R.S., KA
                                              SEQUENCE FROM
                                                                                                      CHLAMYDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-M71;
LIU C.Q., CHIA G.L., DU
SUBMITTED (DEC-1996) TO
EMBL; U78967; G1699049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                     BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMID PND302.
BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CADMIUM RESISTANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P94888;
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                                                                                                                               PCKA.
                                                                                                                                                                                                                                                                                                                                                        422 INYLSIISSLE .:!!! |||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LACTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LACTOCOCCUS LACTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 AYLSTPNSLE 207
:||||::||:
2 SYLSTASSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                   μ.
                                                                                                                                                                                                                                                                                                                                     VSYLSTASSLD
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6;
                                                                                     CHLAMYDIALES;
                                                                                                        TRACHOMATIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / (TREMBLREL.
// (TREMBLREL.
// (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                    PRELIMINARY;
                                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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      KALMAN
                                                                                                                                                                                                                                                                                                                                     11
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SLREL. 03,
SLREL. 08,
E PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     75.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEMBRANE; PHOSPHORYLATION;
398 PHOSPHORYLATION (PROBAI
76466 MW; 6648COBD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33278 MW;
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                                                                                     CHLAMYDIACEAE;
    LAMMEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQ
LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
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                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3FBBB9E2 CRC32;
    O
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ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       50; D
. J
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9.06e+00;
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9.06e+00;
  FAN
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J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROUP; STREPTOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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    MARATHE
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  ARAVIND
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RESULT
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      TRESULTATION OF THE SULTATION OF THE SUL
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Best Local :
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Best Local
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DAVIS R.W.;
"Genome Sequence of a
Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043298;
01-JUN-1998 (
01-JUN-1998 (
01-AUG-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 7
055748
055748;
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01-JUN-1998 (TREMBLREL. 06, LAST SEQUI
01-JUN-1998 (TREMBLREL. 06, LAST ANNO
PUTATIVE RIBONUCLEASE.
CHILO IRIDESCENT VIRUS (CIV) (INSECT VIRUSES; DSDNA VIRUSES, NO RNA STAGE;
SEQUENCE FROM N.A.
ZHANG X., LIU C.-X., LISITSINA M.N.,
SUBMITTED (FEB-1998) TO EMBL/GENBANK,
EMBL; AB007874; D1025766; -.
                                                                                                                                                     ISHIKAWA K., NAGASE T., NAKAJIMA D., SEKI
TANAKA A., KOTANI H., NOMURA N., OHARA O.
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAHR U., TIDONA C.A., DARAI G
VIRUS GENES 0:0-0(1997).
EMBL; AF003534; 62738432; -.
SEQUENCE 292 AA; 33664 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAVIS R.W.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ
EMBL; AE001341; G3329165; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEPHENS R.S., KALMAN S., LAMMEL C. MITCHELL W.P., OLINGER L., TATUSOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               043298
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                                                                                                                                                                                                                                                                                                                                                                                                                              KIAA0414 OR ZNF-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 IPYLTTPESLN 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSYLSTASSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSYLSTASSLD 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TREMBLREL.)
(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLINGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DARAI G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ľ.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9,8,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATUSOV R.L., ZHAO Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 14;
Pred. No. 2.28e+01;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۳
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                                                                                                                                                                                                                                                                                                                                                                      VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8DE1FE30 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            706D89A2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Intracellular Pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; DB 2; 1
No. 1.44e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.L.,
                                     K/DDBJ [
                                                                                                                                                                                                             SEKI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRIDESCENT VIRUS TYPE 6)
: IRIDOVIRIDAE; IRIDOVIRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467
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ZHAO C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                     DATA
                                                                                                                                                        DATA
                                                                 ŝ
                                                                                                                                                                                                                OHIRA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                     LISITSYN
BANKS
                                                                                                                                                        BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRIDOVIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Humans:
                                                                                                                                                                                                                   MIYAJIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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RESULT 10

ID 016568;

AC 016568;

DT 01-JAN-1998
DT 01-JOY-1998
DE F40E12.2 PRO'
GN F40E12.2 PRO'
GN F40E12.3 M
OC CAEMORHABDIT
OC EUKARYOTA; M
OC RHABDITINA; M
OC RHABDITINA; M
RP SEQUENCE FROI
RP SEQUENCE FROI
RP SEQUENCE FROI
RN [1]
RA HILSON R., A
RA BONFIELD J.,
RA GARDNER A.,
RA GARDNER A.,
RA GARDNER A.,
RA GARDNER A.,
RA GARDNER J.,
RA GARSONS J.,
RA SMALDON N.,
RA THIERRY-MIEG
RA WATSON A.,
RT "2.2 Mb of co
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ID 02831;
AC 092831;
DT 01-FEB-1997
DT 01-FEB-1997
DT 01-NOV-1998
DE P/CAF:
GN P/CAF:
GN P/CAF:
OS HOMO SAPIENS
OC EUKARYOTA; M
OC CATARRHINI;
RN [1]
RN [
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Best Local S
Matches
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Best Local
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                 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNIAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TREMBLREL. 05,
01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08,
F40E12.2 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 382:319-324(1996).
EMBL; U57317; G1491937; -.
PFAM; PF00439; bromodomain; 1.
PFAM; PF00583; Acetyltransf; 1.
SEQUENCE 832 AA; 92926 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF049907; G2952308; --
PROSITE; PS00028; ZINC_FINGER_C2H2
ZINC_FINGER; METAL-BINDING; DNA-BII
SEQUENCE 467 AA; 52630 MW; FA6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS EUKARYOTA; METAZOA; NEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A p300/CBP-associated oncoprotein E1A.";
                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96300317
YANG X.J., OGRYZK
                                                                                                                                                                                                                                                                                                          MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 VSYLTAASFLQ 111
||||::|| |:
1 VSYLSTASSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
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Similarity 63.6%;
7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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  contiguous nucleotide
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(TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                          RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETAL-BINDING; DNA-BINDING.
AA; 52630 MW; FA610780 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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actor that
                                                                                                                                                                                                                                                                                                                                                                                                                        DDA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48;
Pred. No.
3; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 4; 1
Pred. No. 2.28e+01;
3; Mismatches 1
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LAST ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1245
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2.28e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ã
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SULT 12

D 061836

C 061836;

T 01-NOV-1996 (TREMBLREL 01, CREATED)

DT 01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)

DE MYELLN BASIC PROTEIN (FRAGMENT).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EF
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AC 01

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SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ
EMBL; AFO16659; G2315574; -.
PFAM; PF00023; ank; 1.
PFAM; PF00533; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDA
NUCLEOPROTEIN (FRAGMENT).
MEASLES VIRUS (SUBACUTE SCLEROSE PANENCEPHALITIS
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGA
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; MORBILLIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o11696
  SEQUENCE FROM N.A. STRAIN-C57BL/6J; TISSUE-BRAIN; MEDLINE; 87118269.
                                                                                                                                                                                                                                                                                        "Identification of three lineages sequence analysis of N, P, M, F, & J. MED. VIROL. 52:113:120; L1997).
EMBL: D87487; D1020995; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOELA D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans.";
NATURE 368:32-38(1994).
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                                                                                                                                                                                                                                                                               NUCLEOPROTEIN.
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45.5%;
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Pred. No. 3.
5; Mismatc
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Pred. No. 2.28e+01
5; Mismatches
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ANNOTATION UPDATE)
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genes in Japan.";
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Q01585; PRELIMINARY;
Q01585; (TREMBLREL 01, CI
01-NOV-1996 (TREMBLREL 01, LI
01-NOV-1996 (TREMBLREL 08, LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEWMAN S., KITAMURA K., CAMPAGNO "Identification of a cDNA coding protein in mouse.";
PROC. NATL. ACAD. SCI. U.S.A. 8:
EMBL; M15062; G19051; -.
PROSITE, PS00559; MYELIN_MBP; 1
ALTERNATIVE SPLICING; MYELIN.
  Q15339;
Q15339;
Q1-NOV-1996
Q1-NOV-1998
                                                                                                                                                                                                                                                                                                                   MGD; MGI:6025; MBP.
MGD; MGI:6025; MBP.
MYELIN; STRUCTURAL PROTEIN; ACETYLATION; METHYLATION;
AUTOIMMUNE ENCEPHALOMYELITIS; ALTERNATIVE SPLICING.
AUTOIMMUNE 105 AA: 21004 MW; 557D83EA CRC32;
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MBP.
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                                                                                                                                                                                                                                                                                                                                                                                                             OF MYELIN.
-!- SUBCELLULAR LOCATION:
EMBL; X67319; G51333; -.
EMBL; L07508; G193587; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6; TISSUE-BRAIN;
MEDLINE; 93186801.
CAMPAGNONI C.W.,
AMUR-UMARJEE S., LANDRY C., HANDLEY V., NEWMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRIMA B., ZELENIKA D., PESSAC B.; "A novel transcript overlapping t J. NEUROCHEM. 59:2318-2323(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57 BLACK;
MEDLINE; 93057537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in cells in the oligodendrocyte lineage in the brain.";
J. BIOL. CHEM. 268:4930-4938(1993).
-i- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KITAMURA K.;
"Structure and developmental regulation of Golli-mbp, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Similarity 66.7%;
6; Conservative
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METAZOA; CHORDATA; VERTEBRATA;
HI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 AA;
  (TREMBLREL.
(TREMBLREL.
(TREMBLREL.
                                                                                  PRELIMINARY;
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10°,
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NA coding for a fifth form
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Pred. No.
3; Misma
CREATED)
LAST SEQUENCE UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 3.58e+01;
3; Mismatches 0
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S., GARBAY
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Best Local s
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est Local Similarity 36.4%;
Matches 4; Conservative
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STRAIN-BES2281;
MEDLINE; 92374852.
MEDLINE; 92374852.
GEISTLICH M., LOSICK R., TURNER J.R., RAU R.N.;
"Characterization of a novel regulatory gene governing the expression of a polyketide synthase gene in Streptomyces ambofaciens.";
MOL. MICROBIOL. 6:2019-2029(1992).
EMBL; X63451; G46702; -
EMBL; X63451; G46702; -
EMBL; X63451; G46702; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 15
Q00510; PRELIMINARY; PRT; 239 AA.
Q00510;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Q1-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 94068468.

MEDLINE: 94068468.

MEDLINE: 94068468.

MCMAHON J., CAMPAGNONI A.T.;

MCMAHON J., CAMPAGNONI A.T.;

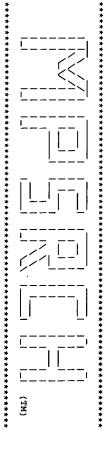
The human myelin basic protein gene is included within a 179-kilobase transcription unit: expression in the immune and cent nervous systems.";

PROC. NATL. ACAD. SCI. U.S.A. 90:10695-10699(1993).

EMBL; L18865; G435060; -

EMBL; L18865; -
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREPTOMYCES AMBOFACIENS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
[1]
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TISSUE-BRAIN;
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3 YLSTASSLD 11
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1 VSYLSTASSLD 11
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Local Similarity 66.7%;
hes 6; Conservation
                                            Sep
                                            2
                                            11:22:14 1999
                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 2; Length 239;
Pred. No. 3.58e+01;
5; Mismatches 2; Indels
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:21:25 1999; MasPar time 2.25 Seconds 150.446 Million cell updates/sec

Sular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-599-226.4 (1-12) from USUB599226.pep 66 1 VSYLSTASSLDX 12

Scoring table:

PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 24.203; Variance 24.721; scale 0.979

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

NO. 1 3 3 4 4 5 5 6 6 6 7 7 7 11 11 11 11 11 11 11 11 11 11 11	SCOTE 525 49 49 49 49 49 49 49 49 49 49 49 49 49	% Query Match 183.3 78.2 74.2 74.2 74.2 74.2 74.2 71.2 71.2 71.2 71.2 71.2 71.2 71.2 71	Length 547 132 471 471 471 12468 1127 1127 1127 1127 1127 1127 1127 112	DB	ID  YDH3_SCHPO MERA_STAAU YW07_MYCTU YW07_MYCTU YW07_MATZE UFO1_MATZE UFO2_MAIZE UFO3_MAIZE UFO3_MAIZE MAPB_MOUSE MAPB_HUMAN MBP_RAT MBP_CAVPO MBP_PANTR MBP_HOMSE MBP_HUMGSE MB	PPPPPGG H H IP	Pred. No. 1.07e-01 5.87e-01 5.87e-01 3.00e+00 3.00e+00 3.00e+00 3.00e+00 3.00e+00 3.00e+00 3.00e+00 8.55e+00 8.
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ω	49	74.2	132	ш	YW07_MYCTU	ICAL 14.7 KD	3.00e+
4	49		468	۳	YPS7_CAEEL		3.00e+
ر.	49		471	۳	UFO1_MAIZE		
σ	49	74.2	471	ب	UFO2_MAIZE	FLAVONOL 3-0-GLUCOSYLT	•
7	49		471	<b>ب</b>	UFO3_MAIZE	FLAVONOL 3-O-GLUCOSYLT	
œ	49		2464	س	MAPB_MOUSE	MICROTUBULE-ASSOCIATED	
9	49		2468	ш	MAPB_HUMAN	MICROTUBULE-ASSOCIATED	•
10	47		127	<u>بــر</u>	MBP_RAT	MYELIN BASIC PROTEIN S	
11	47		167	ب	MBP_CAVPO	BASIC	
12	47		171	<b>}</b> 3	MBP_PANTR	BASIC	
13	47		194	۳	MBP_MOUSE	BASIC	
14	47		196	۳	MBP_HUMAN	BASIC	
15	47		259	1	RNPH_MYCTU	PROBABLE RIBONUCLEASE	
16	47	71.2	259	_	RNPH_MYCLE	PROBABLE RIBONUCLEASE	
17	47	71.2	1107	_	YJEP_ECOLI	HYPOTHETICAL 123.8 KD	
18	46	69.7	152	_	PSAL_GUITH	PHOTOSYSTEM I REACTION	
19	46	69.7	474	<b>J</b> 1	MERA_STRLI	MERCURIC REDUCTASE (EC	1.42e+01
20	46	69.7	485	۳	G6PD_ZYMMO	GLUCOSE-6-PHOSPHATE 1-	1.42e+01
21	46	69.7	541	س	TRPE_VIBPA	ANTHRANILATE SYNTHASE	1.42e+01
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01-JAN-1988 (REL. 06, CREATED) 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE) 01-CCT-1994 (REL. 30, LAST ANNOTATION UPDATE) MERCURIC REDUCTASE (EC 1.16.1.1) (HG(II) REDUCTASE).	ULT 2 MERA_STAAU STANDARD; PRT; 547 AA.	1 VSYLSTASSLD 11	302 VSYLNEASSLE 312	Query Match 83.3%; Score 55; DB 1; Length 352; Best Local Similarity 72.7%; Pred. No. 1.07e-01; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	SEQUENCE 352 AA; 39679 MW; D92A9357 CRC32;	EMBL; Z81317; E276610; HYPOTHETICAL PROTEIN.		an email to license@isb-sib.ch).	l and this statement is not removed. Usag	by non-profit institutio	the Furgory Ricinformatics Institute There are no restrictions on its	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Ricinformatics and the FWRI outstation.		, TO YEAST YNL206C.	MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., CONNOR R.E.;	STRAIN-972;	SEQUENCE FROM N.A.	SCHIZOSACCHAROMYCES.	SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;	STRARYOTA: FINGT: ASCONYCOTA: ARCHTASCONYCETES:		L 39.7 KD PROTE	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)	(REL. 35, CREA		<pre>YDH3 SCHPO STANDARD: PRT: 352 AA.</pre>

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Best Local Similarity
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01-OCT-1996 (REL.
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HYPOTHETICAL 14.7)
MTCY39.07C.
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Q10847;
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"NUCLECTIDE sequence and expression of the mercurial-resistance operon from Staphylococcus aureus plasmid pI258.";

PROC. NATL. ACAD. SCI. U.S.A. 84:5106-5110(1987).

-:- FUNCTION: RESISTANCE TO HG(2+) IN BACTERIA APPEARS TO BE GOVERNED BY A SPECIALIZED SYSTEM WHICH INCLUDES MERCURIC REDUCTASE. MERA PROTEIN IS RESPONSIBLE FOR VOLATILIZING MERCURY AS HG(0).

-:- CATALYTIC ACTIVITY: HG + NADP(+) + H(+) = HG(2+) + NADPH.
    SEQUENCE FROM N.A.
STRAIN-H37RV;
OLIVER K., HARRIS
                                                                              MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA;
ACTINOMYCETALES; CORYNEBACTERINEAE; M
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LADDAGA R.A., CHU L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMID PI258.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
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STAPHYLOCOCCUS AUREUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: HG + NADP(+) + H(+) = HG(2+) + NADPH. COFACTOR: FAD. SUBUNIT: HOMODIMER.

THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.

SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleropean Bioinformatics Institute. There are no resti
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SIMILARITY: CONTAINS A COPY OF THE HEAVY-METAL-ASSOCIATED DOMAIN.
                                                                                                                                                                                                                                                                                                                                                           VSYLSTASSLD
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34, LAST SEQUENT SEQUENT ANNO SECUENT SEQUENT SEQ
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LAST ANNOTATION UPDATE)
PROTEIN CY39.07C.
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      BARRELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52;
Pred. No.
5; Misma
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REDOX-ACTIVE.
FAD (FLAVIN PART) (BY SIMI HG(2+) (POTENTIAL).

HG(2+) (POTENTIAL).
      В
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60DAFC29 CRC32;
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G
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                                                                                   MYCOBACTERIACEAE;
      RAJANDREAM
                                                                                                                                                                                                                                                                          132
                                                                                                      ACTINOBACTERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; L
5.87e-01;
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      м.
А.,
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                                                                                     MYCOBACTERIUM
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Query Match
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RESULT OF THE PROPERTY OF THE 
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Best Local
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Q20085;
15-JUL-1998 (
15-JUL-1998 (
15-JUL-1998 (
                                                                                                                                                                                                            EMBL; 236752; 1
WORMPEP; F35H8
PROSITE; PS0010
PROSITE; PS0010
PROSITE; PS5001
                     DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PUTATIVE SERINE/THREONINE-PROTEIN KINASE F35H8.7
(EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (FEB-1997)
-!- SIMILARITY: WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JONES S.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 274025; E248788; -. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatiche European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed.
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  SEQUENCE
                                                                                                                                                                                      PFAM;
                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED
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EUKARYOTA; METAZOA; NEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F35H8.7
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                                                                                                                                        HYPOTHETICAL PROTEIN; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BERKS M.;
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                                                                                                                    ATP-BINDING
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                                                                                                                                                                  HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASES.
                                                                                                                                                                PF00069;
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PS00107;
PS00108;
PS50011;
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132 AA; 1
                                                                                                                                                                                                       ;; E1346252; -.
H8.7; CE09940.
10107; PROTEIN_KINASE_ATP; 1
10108; PROTEIN_KINASE_DOM; 1
10011; PROTEIN_KINASE_DOM; 1
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  AA,
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121
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THE CONSERVED CATALYTIC DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDA; SECERNENTEA; RHABDITI; RHABDITIDAE; PELODERINAE;
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Pred.
                     PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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  Y SIMILARITY
480A5814 CR
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3.00e+00;
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ng as its content is in
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DDERINAE; CAENORHABDITIS.
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MBL outstation -
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     B S E
                                                                        RESULT
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Best Local Similarity
Matches 8; Conser
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Matches 6; Conser
UFO2_MAIZE
P16165;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88284304.

RALSTON E.J., ENGLISH J.J., DOONER H.K.;

"Sequence of three bronze alleles of maize and correlation with "
genetic fine structure.";

GENETICS 119:185-197(1988).

-i- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS,

-i- TUNCTURATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MCC ALLELE).
BZ1 OR UGT71A1.
                                                                                                                                                                                                                                                                                                                                                      TRANSFERASE;
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                           MAIZEDB; 13885; -.
PROSITE; PS00375; UDPGT; 1.
PFAM; PF00201; UDPGT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S01052; S01052.
PIR; S08324; S08324.
MAIZEDB; 13885; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X13500;
EMBL; X07940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 88284304.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZEA MAYS (MAIZE).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACI
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UFO1_MAIZE P16166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTHOCYANIN BIOSYNTHETIC PATHWAY.
SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: UDP-GLUCOSE + A FLAVONOL - UDP + FLAVONOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-O-D-GLUCOSIDE.
PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSYLSTASSL 10
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                                                                                                                                                 VSYLSTASSL
                                                                                                                                                                                                                                                                                                                                                    E; GLYCOSYLTRANSFERASE.
471 AA; 48769 MW; 8P
  (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G1030071; -
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Conservative
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  14, CREATED)
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Pred. No.
2; Misma
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                                                 471
                                                                                                                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                                                                                                                Length 471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRACHEOPHYTA;
SIDA; POALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTHOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Zea mays.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JR.;
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Best Local
                                                                                                                                                                                                                                                                                                                     UFO3_MAIZE
P16167;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ULTAFK-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MC2 ALLELE).
BZ1 OR UGT71A1.
SEQUENCE FROM N.A.

MEDLINE; 88284304.

RALSTON E.J., ENGLISH J.J., DOONER

"Sequence of three bronze alleles
genetic fine structure.";
GENETICS 119:185-197(1988).
                                                                                                                                                                                                            BZ1 OR UGT71A1.
ZEA MAYS (MAIZE).
EUKARYOTA; VIRIDIPLANTAE;
                                                                                                                                                                                                                                                      01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE FLAVONOID
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-W22 ALLELE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAIZEDB; 13885; -...
PROSITE; PS00375; UDPGT; 1.
PFAM; PF00201; UDPGT; 2.
TRANSFERASE; GLYCOSYLTRANSFERASE.
SEQUENCE 471 AA; 48621 MW; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FURTEK D., SCHIEFELBEIN J.W., JOHNSTON F., NELSON O.E. JR.; "Sequence comparisons of 3 wild-type bronze-1 alleles from Zea rplant mol. BIOL. 11:473-481(1988).

-i- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYAN.
                                                                                                        SEQUENCE FROM N.A.
FURTER D., SCHIEFELBEIN J.W., JOHNSTON
"Sequence comparisons of 3 wild-type br
PLANT MOL. BIOL. 11:473-481(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZEA MAYS (MAIZE).
EUKARYOTA; VIRIDIPLANTAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUPHYLLOPHYTES;
                                                                                                                                                                                                  EUPHYLLOPHYTES;
                                                                                                                                                                                    OACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 80.0% nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         46 LSFLSTASSL
                                                                                                                                                                                                                                                                                                                                                                                                               1 VSYLSTASSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTHOCYANIN BIOSYNTHETIC PATHWAY.
SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X13501;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; G295854;
S08325.
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                                                                                                                                                                                                  SPERMATOPHYTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREPTOPHYTA; EMBRYC HYTA; MAGNOLIOPHYTA;
                                                                                                                                                                                                STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; HYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
                                DOONER H.K.;
lleles of maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
2; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49;
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Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                    471
                                                                                                                         bronze-1
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                                                                                                                                                                                                                                                                                                                                                    B
                                  and correlation with
                                                                                                                         NELSON O.E.
e-1 alleles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UDP + FLAVONOL
                                                                                                                          from
                                                                                                                                       JR.;
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Best Local S
Matches
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J. CELL BIOL. 109:3367-3376(1989).

J. CELL BIOL. 109:
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PROSITE; PSO0375; UDPGT; 1.
PRAM; PF00201; UDPGT; 2.
TRANSFERASE; GLYCOSYLTRANSFERASE.
SEQUENCE 471 AA; 48673 MW; 4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities
or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X13502; G22506; -. EMBL; X07937; G22210; -. PIR; S01037; S01037. PIR; S08326; S08326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The microtubule binding of MAP1B contains a repeated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-SWISS WEBS!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP1B OR MTAP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOBLE M., LEWIS S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 90094539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P14873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 LSFLSTASSL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ.
                                                                                                  STABILIZING MICROTUBULES.
SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, (WITH MAP1A AND MAP1B PROTEINS.
DOMAIN: HAS A HIGHLY BASIC REGION WITH MANY COPIES OF KKEE AND KKEL/V, REPEATED BUT NOT AT FIXED INTERVALS.
REGION IS RESPONSIBLE FOR THE BINDING OF MAP1B TO MICH BOTH IN VITRO AND IN VIVO.
PTM: LC1 IS COEXPRESSED WITH MAP1B. IT FROM MAP1B BY PROTECTIVIC PROCESSING. BOTH MAP1A AND MAP1B. IT INTERACTS WIT OF MAP1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-O-D-GLUCOSIDE.
PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: UDP-GLUCOSE + A FLAVONOL - UDP + FLAVONOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, T GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTHOCYANIN BIOSYNTHETIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.2%;
larity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEBSTER; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COWAN N.J.;
ing domain of microtubule-associated protein
ated sequence motif unrelated to that of MAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 1; I
Pred. No. 3.00e+00;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                            WITH THE
                                                IT IS A POLYPEPTIDE GENERATED G. IT IS FREE TO ASSOCIATE WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAMMALIA; EUTHERIA; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                         AMINO-TERMINAL REGION
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                                                                                                                                  MICROTUBULES
                                                                                                                                                                                    OF THE SEQUENCE
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                                                                                                                                                           LATTER
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RESULT
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RT identification of a related gene on chromosome 15.";

RT GENOMICS 22:273-280(1994).

CC :-- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST CC TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS CC MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN CC :-- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE CC SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAP1A AND MAP1B PROTEINS.

CC WITH MAP1A AND MAP1B PROTEINS.

CC WITH MAP1A AND MAP1B PROTEINS.

CC REGION IS RESPONSIBLE FOR THE BINDING OF MAP1B TO MICROTUBULES CONTROL TN UTEND AND TN TWO TOO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.2%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                             MAP1B.
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                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                              P46821;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     LIEN L.L.,
                                                                                                                                                                                                   MEDLINE; 95104835.
                                                                                                                                                                                                                                                                                           MICROTUBULE-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:97179; MTAP5.
ITE; PS00230; MAP1B_NEURAXIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S07549; QRMSP1
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                                                                                                                                                                                       FEENER C.,
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(REL. 32, LAST SEQUENCE UP
(REL. 37, LAST ANNOTATION
-ASSOCIATED PROTEIN 1B [CON
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Pred. No. 3.00e+00
3; Mismatches
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LYS-RICH (HIGHLY BASIC, CONTAINS MANY
KKEE AND KKEI/V REPEATS).
12 X 17 AA TANDEM REPEATS.
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                                                                                                                                                            , KUNKEL L.M.;
ciated protein lr
n chromosome 15.
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Best Local Similarity
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21-JUL-1986 (REL. 01,
01-NOV-1997 (REL. 35,
MYELIN BASIC PROTEIN S
                                                                                      BIOL.
                                                                                                                           SEQUENCE;
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P02688;
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                                                                                                                                                            RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
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                          ROACH A., BOYLAN K., HORVATH S. "Characterization of cloned comprotein: absence of expression CELL 34:799-806(1983).
                                                                                                                                                     RODENTIA;
                                                                                                                                                                               MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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        SEQUENCE
                                                             MEDLINE; 84026484
                                                                      SEQUENCE
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SIMILARITY: TO NEURAXIN.
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                                                                                        CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00414; MAP1B_neuraxin;
                                                                                      M. BUDZINSKI R.M., STOFFEL W.;
proteolipid protein and myelin basic protein
iption of the two genes during myelination.";
HEM. HOPPE-SEYLER 367:825-834(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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75127359
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01, LAST SEQ
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60.0%;
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                                                                                                                                                     MURIDAE;
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LYS-RICH (I
KKEE AND KK
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110.
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AE; MURINAE;
                                                                                                                                                                                                                                    PRT;
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                                          PRUSINER S.B., HOOD L.E.;
representing rat myelin basic
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No. 3.00e+00;
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17 AA TANDEM REPEATS.
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RATTUS.
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01-MAY-1992 (REL. 22, CREATED)

01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)

101-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)

101-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)

21 MYELIN BASIC PROTEIN (MBP).

22 CAVIA PORCELLUS (GUINEA PIG).

23 EUKARYOTA; METAKOA; CHORDATA; VERTEBRATA; MAI

24 EUKARYOTA; METAKOA; CHORDATA; CAVIIDAE; CAVIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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BIOCHEM. J.
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INIT_MET
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CONFLICT
SEQUENCE
                                                                                                                                              SEQUENCE.
MEDLINE; 8
DEIBLER G.
"Sequence
SHAPIRA R., MCKNEALLY S.S., CHOU F., KII "Encephalitogenic fragment of myelin bas sequence of bovine, rabbit, guinea pig, J. BIOL. CHEM. 246:4630-4640(1971).
                                                                                                                                                                                                                                                                                                                                                                                           MBP_
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Sequence of g
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B24351; B24351.
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73180720.
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. 43:100-105(1984).
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ACETYLATION; METHYLATION;
S; ALTERNATIVE SPLICING.
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SG -> GS (IN REF. 4).
M -> I (IN REF. 2).
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                                                                                                                                              KRUTZSCH H.C.,
n basic protein
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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834FEBF5 CRC32;
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                                                     KIBLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; L
8.55e+00;
                                IBLER R.F.;
asic protein.
, monkey, and
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01-OCT-1996
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01-JAN-1988
01-FEB-1996
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SEQUENCE
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P06906;
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LIFE SCI. 1
                RODENTIA;
                            EUKARYOTA;
                                      MBP.
MUS MUSCULUS (MOUSE)
                                                               MYELIN
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EUKARYOTA; METAZOA; CHORDATA;
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WESTALL F.C
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SUBCELLULAR LOCATION: CYTOPLASMIC
R A37246.
R C92087; C92087.
SSITE; PS00569; MYELIN_MBP; 1.
DSTIE; PS00569; MYELIN_MBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                      npanzee brain.";
E SCI. 17:219-223(1975).
FUNCTION: THIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                             YLATASTMD
                                                                                                                                                                                                                                                                                                                                                                                OF MYELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                        proposed sequence
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                                                                BASIC
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Similarity 66.7%;
6; Conservative
                                                                                                                                                                                                                              Similarity 6; Conse
                                                                                                                                                                                                                                                                                                                               PS00569; MYELIN_MBP; STRUCTURAL PROTEIN; AC
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                SCIUROGNATHI;
                                                                                                                                                                                                                                                                           107
171
                             METAZOA;
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                                                             (REL. 04, CREATED)
(REL. 05, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDAT
C PROTEIN (MBP).
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LAST ANNOTATION
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                MURIDAE;
                                                                                                                                                                                                                                                                             MW;
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Pred. No. 3; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                          KALTER
                                                                                                                                                                                                                                                                                                                               ACETYLATION; METHYLATION;
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Pred. No. 8.55e+00;
3; Mismatches 0
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METHYLATION
SIMILARITY).
                                                                                                                                                                                                                                                                                         ACETYLATION.
METHYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCES EXPERIMENTAL ENCEPHALOMYELITIS.
               VERTEBRATA; MAMMALIA;
AE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                             encephalitogenic
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No. 8.55e+00;
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                                                                                                                                                                                                                                                    Length 171;
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                           EUTHERIA;
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  TAKAHASHI N., ROACU
"Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ALL MEDLINE; 86079555.

DE FERRA F., ENGH H., H LAZZAKINI R.A.;
"Alternative splicing a
 EMBL;
EMBL;
EMBL;
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                                                                                                  EMBL;
EMBL;
EMBL;
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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.";
CELL 43:721-727(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYEL-
-i- ALTERNATIVE PRODUCTS: MOUSE HAS FOUR FORMS OF
17KD, AND 14KD, PRESENT IN RELATIVE AMOUNTS OF
4 FORMS ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- THE SEQUENCE SHOWN IS THAT OF THE 21.5KD FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse: one gene can encode
use of exons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of protein in mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-23 F
MEDLINE; 89252919.
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M115291
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M115331
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TAKAHASHI N., ROACH A., TEPLOW D.B., PRUSINER S.B "Cloning and characterization of the myelin basic mouse; one gene can encode both 14 kd and 18.5 kd
84:886-890(1987).
                                                                                                                                                                                                                                                                                                                                   KAMHOLZ J.,
                               fifth form
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                                of myelin basic
                                                                                                                                                      protein gene from MBPs by alternate
                                                                                                                                                                                          HOOD L.;
                                                                                                                                                                                                                                                                                                                                   C.,
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                                                                                                                                                                                                                                                                                                                                   MOLINEAUX
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SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EW (See http://www.isb-sib There are no rest Usage and the ý restrictions and EMBL outstation a collaboration 9

S OF MBP

gene

STRUCTURE

OF MBP, 21.5KD, OF 1:10:3.5:35.

18.5KD THOSE

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   Query Match
Best Local S
Matches
                                                                                            MEDLINE: 86308101.
ROTH H.J., KDOWN
SEQUENCE OF 1-58 ANI
MEDLINE: 86.259.714.
KAMHOLZ J., DE FERRI
"Identification of 1
cloning.";
PROC. NATL. ACAD. S
                                                                                                                                                                                                                                                                                                                      21-JUL-1986
01-NOV-1991
01-JUL-1993
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VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                               MYELIN
                                                                                                                                                                                                                                                                                                                                                           MBP_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYELIN; STRUCTURAL PROTEIN; ACETYLATION; NATIONAL AUTOIMMUNE ENCEPHALOMYELITIS; ALTERNATIVE
                                                              "Isolation and characterization of a cDNA coding 17.3K myelin basic protein (MBP) variant."; J. NEUROSCI. RES. 16:227-238(1986).
                                                                                                                                                the
                                                                                                                                                                         ROTH H.J., KRONQUIST
                                                                                                                                                                                 SEQUENCE FROM N.A
MEDLINE; 87311781
                                                                                                                                                        "Evidence for the expression of four myelin
                                                                                                                                                                 CAMPAGNONI A.T.
                                                                                                                                                                                                                                                                                                                                                                                                        12 YLATASTMD
                                                                                                                                      e developing human spinal cord
NEUROSCI. RES. 17:321-328(1987
                                                                                                                                                                                                                                                                                                                                                                                               3 YLSTASSLD 11
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100399 G387419;
100399 G387419;
100400 G387419;
100401 G387419;
100402 G387419;
100403 G387419;
100403 G387419;
100403 G387419;
100403 G387419;
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A26591; A26591.
B26591; B26591.
                                                                                                                                                                                                                      organization of the the mouse gene.";
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STRUCTURAL PROTEIN; ACETYLATION; METHYLATION;
                                    0F 1-58 &
86259714.
                                                                                                                                                                                                             mouse gene.";
EM. HOPPE-SEYLER
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194
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(REL.
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larity 66.7%;
Conservative
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   U.S.A.
                                               -196
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                  PUCKETT C., LAZZARINI forms of human myelin
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METHYLATION (BY SIMILARITY).
MISSING (IN 18.5 KD FORM AND 1.
MISSING (IN 17 KD FORM AND 14.)
MISSING (IN 2.586D9A74 CRC32;
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3; M
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  83:4962-4966(1986)
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8.55e+00;
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cDNA cloning.";
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                   protein
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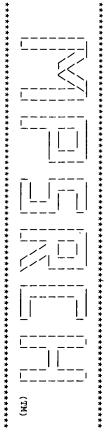
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[5]
SEQUENCE OF 1-58 AN MEDLINE; 72066400.
CARNEGIE P.R.;
VARSPLIC
SEQUENCE
                                                                          INIT_MET
MOD_RES
MOD_RES
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 45-58 AND 85-114, REVISIONS.
SHAPIRA R., MCKNEALLY S.S., CHOUF., KIBLER R.F.;
"Encephalitogenic fragment of myelin basic protei sequence of bovine, rabbit, guinea pig, monkey, a J. BIOL. CHEM. 246:4630-4640(1971).
                                                                                                                                                                             EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                  EMBL;
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-!- FUNCTION: THIS PROTEIN MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOYLAN K.B., AYRES T.M., POP
PRUSINER S.B.;
"Repetitive DNA (TGGA)n 5' t
new form of oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Amino acid myelin.";
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BALDWIN G.S., CARN
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                                                                                                                                                                                                                                                                                                            entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphism.";
GENOMICS 6:16-22(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                            VARSPLIC
                                               DOMAIN
                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHYLATION
                                                                                                                   AUTOIMMUNE
                                                                                                                              MYELIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>6</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                          olation and partial characterization of methylated encephalitogenic basic protein of myelin."; CHEM. J. 123:69-74(1971).
                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the El Buropean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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ALTERNATIVE PRODUCTS:
(THE MOST ABUNDANT), I
                                                                                                                                                                           M3577; G307160;
M30515; G307161;
M30515; G307161;
M30047; G307159;
X17286; E221974;
X17287; E221974;
X17790; E221974;
X17798; E221974;
X17788; E221974;
X17789; E221974;
X17789; E221974;
X17789; E221974;
X17789; E221974;
                                                                                                                                                                                                                                                                                                                                                                                                                        OF MYELIN
                                                                                                                                                          A24153; MBHUB.
S10482; S10482.
                                                                                                                               STRUCTURAL
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                                                                                                                             PS00569; MYELIN_MBP;
STRUCTURAL PROTEIN; A
                                                                                                                                                                                                                                                                                                  requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    non-profit institutions as long as and this statement is not removed. U
                                                                                                                  ENCEPHALOMYELITIS;
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HUMANS HAVE THREE FORMS OF MBP,
AND 17.2K. THE THREE FORMS ARE P
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                                                                                                                  ACETYLATION; | S; ALTERNATIVE
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                                                       METHYLATION (MONO-:6% OR DI-:60%).
INDUCES EXPERIMENTAL AUTOIMMUNE
ENCEPHALOMYELITIS IN MONKEYS, RABBITS,
AND RATS BUT NOT IN GUINEA PIGS.
         MISSING
                           ENCEPHALOMYELITIS MISSING (IN 18.5
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Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                       EMBL; 273902; E245034; -.
EMBL; 27555; E250346; -.
PROSITE; P501277; RIBONUCLEASE_PH; 1.
PPAM; PF01138; RNASE_PH; 1.
TRANSFERASE; NUCLEOTIDYLTRANSFERASE; TRNA PROCESSING.
SEQUENCE 259 AA; 27351 MW; 89F9EFE6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-H37RV:
MURRHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
MURRHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: RNASE PH IS A PHOSPHOROLYTIC EXORIBONUCLEASE THAT
REMOVES NUCLECOTIDE SESIDUES FOLLOWING THE -CROATEMUNUS OF T
AND ADDS NUCLECOTIDES TO THE ENDS OF RNA MOLECULES BY USING
NUCLEOSIDE DIPHOSPHATES AS SUBSTRAIES (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: TRNA(N+1) + ORTHOPHOSPHATE = TRNA(N) +
A NUCLEOSIDE DIPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNPH_MYCTU
Q10628;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDYLTRANSFERASE).
RPH OR MTCY130.25 OR MTCY02B10.04.
MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOY-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROBABLE RIBONUCLEASE PH (EC 2.7.7.56) (RNASE
                                                                                                              143 VTYLSAAGKL 152
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                     2 11:21:33 1999
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Pred. No. 8.55e+00;
3; Mismatches 1
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Pred. No. 8.55e+00;
3; Mismatches 0;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:20:54 1999; MasPar time 3.25 Seconds 147.929 Million cell updates/sec

Title: >US-08-599-226-4
Description: (1-12) from US08599226.pep
Perfect Score: 66
Sequence: 1 VSYLSTASSLDX 12

uence: 1 VSYLSTASSLDX 12
ring table: PAM 150

Scoring table: PAM 150 Gap 15

earched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60

pir60
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 23.694; Variance 27.579; scale 0.859

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

49 74.2 599 2 49 74.2 2464 2 49 74.2 2464 2 48 72.7 292 2 47 71.2 167 2 47 71.2 167 2 47 71.2 197 1 47 71.2 239 2 47 71.2 259 2 47 71.2 259 2 47 71.2 328 1 47 71.2 328 1 47 71.2 328 1 47 71.2 1107 2 46 69.7 133 2	Sult 10. 22 3	Score 52 51 50 49 49	γς:	(	DB 2	E29504 S60941 D70108 H70759 A71645 S08325 S01057	Description  mercury(II) reductase probable membrane pro conserved hypothetical protein hypothetical protein protein 934 (p34) RP8 flavonol 3-O-glucosyl flavonol 3-O-glucosyl flavonol 3-O-glucosyl flavonol 3-O-glucosyl
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probable membrane pro	protein-tyrosine kina	probable acrAl protei	probable membrane pro	mercury(II) reductase		DNA-binding protein C	hemagglutinin precurs	hypothetical protein	hypothetical protein	hypothetical 43.4 kD	hypothetical protein	probable glucose 1-de	ORF 3' to arbB - Erwi	ybhJ protein - Escher	ferric vibriobactin r	CTP synthase (EC 6.3.	membrane protein 4.1	anthranilate synthase	anthranilate synthase	glucose-6-phosphate 1	mercur) (II) renuccase
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ATE_	Db 235 VDYLTSTSALE         : :   :   :   Qy	Query Match Best Local Simi Matches 5;	89-528 SUMMARY	FEATURE	#gene #genome CLASSIFICATION KEYWORDS	GENETICS	<pre>#accession E29504 ##molecule_type DNA ##residues 1-5</pre>	#cross-referer	#journal #title	#authors	ACCESSIONS REFERENCE	ALTERNATE_NAMES ORGANISM DATE	RESULT 1 ENTRY TITLE
\$60941 #type complete probable membrane protein YOR214c - yeast (Saccharomyces cerevisiae) hypothetical protein O5022; hypothetical protein YOR50-4 #formal_name Saccharomyces cerevisiae 15-reb-1996 #sequence_revision 01-Mar-1996 #text_change 05-Jun-1998	SALE 245  : :  SSLD 11	h 78.8%; Score 52; DB 2; Length 547; Similarity 45.5%; Pred. No. 2.07e+00; Conservative 5; Mismatches 1; Indels 0; Gaps 0;	#domain dihydrolipoamide dehydrogenase homology #label DLD #length 547 #molecular-weight 58565 #checksum 1158	#domain heavy-metal-associated homology #label HMA\	merA plasmid plasmid #superfamily Bacillus mercury(II) reductase; dihydrolipoamide dehydrogenase homology; heavy-metal-associated homology disulfide bond; FAD; oxidoreductase		_type_DNA _type_DNA 1-547 ##label_LAD	resistance operon from Staphylococcus aureus plasmid p1258. #cross-references MUID:87260937	Nucleotide sequence and expression of the mercurial	a, R.A.; Chu, L.; Misra, T.K.;	E29504 A94170	Hg(11) reductase; mercuric reductase #formal_name Staphylococcus aureus 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Dec-1998	

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Best Local Similarity 60.0%;
Matches 6; Conservative
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217-233
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#journal Yeast (1996) 12:877-885

#title Sequence and analysis of a 33 kb fragment from the right

#cross-references MUID:96437977

#accession S71716
                                           #journal #title
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##residues 1-236 ##label BOY
##cross-references EMBL:Z75122; N
##cross-references S286
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##note the nucleotide sequence was submitted to the EMBL
Library, October 1995
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##cross-references EMBL:X92441; NID:g1050762;
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                                Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.;
Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb,
J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.;
Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman,
J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst,
K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.
Nature (1997) 390:580-586
Genomic sequence of a Lyme disease spirochaete, Borrelia
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Sequence and analysis of a 33 kb fragment from the right
of chromosome XV of the yeast Saccharomyces cerevisiae
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$60938
Galisson, F.; Dujon, B
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05-Jun-1998
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                                                                                                                                                                                                                                                                                                                                                            #formal_name Borrelia burgdorferi #common_name Lyme disease
    spirochete
                                                                                                                                                                                                                                                                                                                                                                                                                         D70108 #type complete conserved hypothetical protein BB0068 - Lyme disease
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                     burgdorferi
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pth 236 #molecular-weight 26156 #checksum 8999
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Pred. No. 3.40e+00;
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Best Local Similarity 60.0%;
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                     #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ###Cross-references GB:Z74025; GB:AL123456; NID:g3261586; PID:e248788; ##cross-references GB:Z74025; GB:AL123456; NID:g3261586; PID:e248788;
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TIGR:BB0068
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Nature (1998) 393:537-544
Deciphering the biology of Mycobacterium tuberculosis from
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                                                                                             #Type complete
protein p34 (p34) RP832 - Rickettsia prowazekii
#formal_name Rickettsia prowazekii
21.Nov-1998 #sequence_revision 21-Nov-1998 #tex
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17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
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                     Andersson,
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 Sicheritz-Ponten,
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Pred. No. 8.
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Pred. No. 5.54e+00;
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8.98e+00
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A.; Andersson, J.O.;
U.C.M.; Podowski, R.M.;
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Best Local Similarity 80.0%;
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##cross-references GB:AJ235273; GB:AJ235269;
PID:g3861358
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                                                $01052 *type complete flavonol 3-0-glucosyltransferase (EC 2.4.1.91) (allele Bz-MCC) - maize (DD9Jucose flavonoid glucosyltransferase #formal_name Zea mays #common_name maize 31-Dec-1990 *sequence_revision 31-Dec-1990 *text_change 08-Sep-1997
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The genome sequence of Rickettsia of mitochondria.
A71645
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S01037
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glycosyltransferase; hexosyltransferase
*length 471 *molecular-weight 48621 *check
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#length 300 #molecular-weight 34582
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 E.J.; English, J.J.;
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Pred. No. 8.98e+00;
2; Mismatches 0;
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Pred. No. 8.98e+00;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                             #authors Ralston, E.J.; English, J.J.; Dooner, H.K.
#journal Genetics (1988) 119:185-197
#title Sequence of three bronze alleles of maize and
with the genetic fine structure.
#cross-references MUID:88284304
#accession S01037
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#title Sequence of three bronze alleles of maize and with the genetic fine structure.
#cross-references MUID:88284304
#accession S01052
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##cross-references EMBL:X07937; NID:g222209; PID:g222210
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Similarity 80.0%;
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glycosyltransferase; hexosyltransferase
#length 471 #molecular-weight 48769 #check
                  175/1
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Sequence comparisons of three wild-type Bronze-1 alleles from Zea mays.
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Sequence comparisons of three wild-type Bronze-1 alleles from
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#superfamily flavonol 03-glucosyltransferase
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R.; Atavind, L.; Mitchell, W.P.; Olinger, L.; Tatusov,
R.L.; Zhao, O.; Koonin, E.V.; Davis, R.W.
Science (1998) 282:754-759
Genome sequence of an obligate intracellular pathogen of
humans: Chlamydia trachomatis.
                                                                                                                                                                                  #title Identification of two distinct microtubule binding domains recombinant rat MAP 1B.

#cross-references_MUID:92347374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #accession
                                                                                                                                                                  #accession
                                                                                                                                                                                                                                                          #authors
                                                                    ##residues 1-2364 ##label ZAU
##cross-references GB:X60550
##experimental_source brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
1-599 ##label ARN
##rrestdues 1-599 ##label ARN
##cross-references GB:AE001341; GB:AE001273; NTD:g3329156; PID:g3329165
##cxperimental_source scrotype D, strain UW-3/Cx
                                                                                                               ##molecule_type mRNA
##residnee
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Local Similarity 54.5%;
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                                                                                                                                                                A56577
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#superfamily phosphoenolpyruvate carboxykinase (GTP)
#length 599 #molecular-weight 66244 #checksum 5490
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hexosyltransferase
#length 471 #molecular-weight 48673 #checksu
                                                                                                                                                                                                                                                                                                                microtubule-associated protein MAP 1B - rat (fragment) #formal_name Rattus norvegicus #common_name Norway rat 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Feb-1997
not complete
#superfamily microtubule-associated protein MAP1B
#length 2364 #checksum 9159
                                                                                                                                                                                                                                         Zauner, W.; Kratz, J.; Staunton, J.; Eur. J. Cell Biol. (1992) 57:66-74
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                                                   nucleotide sequence not given; conceptual translation
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4; Misma
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2; Mismatches
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Pred. No. 8.98e+00;
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity 60.0%;
Matches 6; Conservative
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#journal J. Cell Biol. (1989) 109:3367-3376
#title The microtubule binding domain of microtubule-associated protein MAPIB contains a repeated sequence motif unrelated to that of MAP2 and tau.
#cross-references MUID:90094539
#accession S07549
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1208,1662,1877,
1918,2003,2030,
2054,2083
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660-663,668-671,
674-677,679-682,
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1563,1702,1708,
1990,2057,2063,
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691-694,695-698,
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##cross-references EMBL:X51396; NID:g52999; PID:g53000
##CICATION #superfamily microtubule-associated protein
RDS microtubule binding; phosphoprotein; tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 ISYLASVSSL 376
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23,727-730,
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                     12
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predicted\
#binding_site phosphate (Tyr) (covalent) #status
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#region 17-residue repeats\
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MTB\
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#type complete
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                                                                                                                                               Score 49; DB 1;
Pred. No. 8.98e+00
3; Mismatches
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Pred. No. 8.98e+00;
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                                                      #authors
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                                                                                                                                                                                                                                                                                             394 ISYNSTSSSLE 404
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# #length 292 #molecular-weight 33664 #checksum 532
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Local Similarity 45.5%;
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                                                                                                  myelin basic protein S - rat
small myelin basic protein
formal_name Rattus norvegicus #common_name Norway rat
24 Apr-1984 #sequence_revision 08-Feb-1996 #text_change
05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A p300/CBP-associated factor that adenoviral oncoprotein ElA.
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The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391; similarities in coding strategy between insect and vertebrate iridoviruses.
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#formal_name Chilo iridescent virus
24_Mar-1999 #sequence_revision 24-Mar-1999 #text_change
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Schaich, M.; Budzinski, R.M.; Stoffel, W.
Biol. Chem. Hoppe-Seyler (1986) 367.825-834
Cloned proteolipid protein and myelin basic protein
Transcription of the two genes during myelination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature (1996) 382:319-324
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Nakatani,
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P/CAF protein - human
P/CAF protein - human
#formal_name Homo sapiens #common_name man
12_reb_1988 #sequence_revision 13-Mar-1998 #text_change
                                                                                      B24351; A90275; A94243; A21062;
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#molecular-weight 92926 #checks
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Pred. No. 1.45e+01;
3; Mismatches 1
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Pred. No. 1.45e+01;
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#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal
#title
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#accession A21062
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#cross-references MUID:75127359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##experimental_source strain Sprague-Dawley
IFICATION #superfamily myelin basic protein
alternative splicing; blocked amino end; experimental
autoimmune encephalomyelitis; methylated amino acid; myelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type protein
##residues 2-128 ##label
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                                                                                                                                                                   YLSTASSLD
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A37246 #type complete
myelin basic protein - guinea pig
myelin Al protein
#formal_name Cavia porcellus #common_name guinea pig
31-Jul-1991 #sequence_revision 31-Jul-1991 #text_char
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Experimental allergic encephalomyelitis to encephalitogenic proteins and peptices MUID:73180720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunkley, P.R.; Carnegie, P.R.
Biochem. J. (1974) 141:243-255
Amino acid sequence of the smaller
                                                                                                                                                                                                                                                                                                                    experimental #length 128 #molecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Characterization of cloned cDNA representing rat myelin basic protein: absence of expression in brain of shiverer mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roach, A.; Boylan, K.; Horvath,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A94243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A94243
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                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2-128 ##label DUN
at position 105, arginine, monomethylarginine, and
dimethylarginine occur in the ratio 4:4:1
rats have two myelin basic proteins; the smaller one,
shown above, is missing 40 residues (following residue
114 or 115) with respect to the larger ones from other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the sequence reported for this encephalitogenic peptide differs from that shown by a transposition of residues 47 and 48; two other differences are printing errors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
46-86 ##label MCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-124,'I',126-128 ##label ROA
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                                                                                                                                                                                                                                                                                                                                                           #modified_site omega-N.methylarginine or omega-N,
    omega-N'-dimethylarginine (Arg) (partial) #status
                                                                                                                                                                                                                                                                                                                                                                                                    #modified_site blocked amino end (Ala) (in mature form)
  (probably acetylated) #status experimental\
                                                                                                                                                                                                                                                                                                                                                                                                                                                           #product myelin basic protein S #status experimental
                                                                                                                                                                                                                                                             71.2%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             #label MAT
                                                                                                                                                                                                                                                                                                                    #molecular-weight 14211 #checksum
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                                                                                                                                                                                                                                        Score 47; DB 1;
Pred. No. 2.31e+01
3; Mismatches
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peptides.
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      #text_change
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

9 9 1 Thu Sep 2 11:22:32 1999; MasPar time 1.38 Seconds 88.032 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Sequence: >US-08-599-226-4 (1-12) from USOB599226.pep 66 1 VSYLSTASSLDX 12

Scoring table: PAM 150 Gap 15

106580 seqs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 15.730; Variance 46.168; scale 0.341

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID			Pred. No.
_	48	72.7	426	ω	PCT-US95-1	Sequence 2,	Applicatio	
2	48	72.7	426	μ	08-336	equence 2	ati	P T
w	47	1.	20	N	US-08-468-	N	cat	
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σ	47		170	N	US-08-327-	Sequence 1,	Applicatio	
7	45	8	345	N	-08-44	40	lica	
8	45	8	384	Н	-08-4	5,	Applicatio	٠.
9	44	6.	170	4	5194425-3	Patent No. 5	194425.	
10	44		170	N	-08-2	Sequence 1,	Applicatio	
11	43	Ņ	209	N	-08-7	2,	Applicatio	
12	43	.5	822	N	-80-	7,	,	
13	43	.5	913	۲	-08-2	e 6,	Applicatio	
14	43		913	۲	-80-	e 6,	Applicatio	
15	43		25	N	US-08-356-	e 2,	Applicatio	
16	43	5	25	2	Ĺ	е 8,	Applicatio	
17	43	ŗ	25	N	US-08-414-	e 68	Ħ	
18	43	5	1255	N	US-08-486-	e 68	Applicati	
19	43	ŗ	25	N	N	e 2,	Applicatio	
20	43	ŗ	25	N	-46	e 68	Ħ	
21	43	5	25	<b>ب</b>	$\boldsymbol{\sigma}$	e 68	Applicati	
22	43	5	99	N	US-08-222-	e 12	Applicati	
23	43	5	72	N	Ν	27	Applicati	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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T-US	US-08-413-	US-08-220-	PCT-US91-0	US-07-688-	US-08-852-	us-08-712-	us-09-057-	5395759-2	US-08-337-	US-08-588-	US-08-452-	US-08-753-	PCT-US95-1	5468481-3	PCT-US96-0	PCT-US96-0	US-08-118-	PCT-US93-0	US-08-118-	PCT-US93-0	US-08-222-
101, Appli	, Applica	, Appli	e 16, App	Sequence 16, Applicati	2, App	3, Appl	Sequence 7, Applicatio	o. 5395759.	2, Appl	'n		2, Appl	Sequence 2, Applicatio	Patent No. 5468481.	Ņ	9, A	e 248,	Sequence 248, Applicat	e 111, Ap	e 111	Sequence 2, Applicatio
2.95e+02		ω.	س	2.31e+02										٠.,		2.31e+02	ω	ພ	2.31e+02	2.31e+02	1.81e+02

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STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE 426 AA; 47234 MW; 1032622 CN;	H: 4	TION INFORMATI (908) 594-673 908) 594-4720	CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: CARTY, CHRISTINE E. REGISTRATION NUMBER: 36,099 REFERENCE/DOCKET NUMBER: 19211Y	25232	RAHWAY  NEW JERSEY  1 USA 17065-0907  READABLE FORM: TYPE: Flopby disk	Sequence 2. Application PC/TUS9513795 GENERAL INFORMATION: APPLICANT: HOLLIS, GREGORY F. APPLICANT: PATEL, MAYUR D. TITLE OF INVERTION: DNA ENCODING CANINE IMMUNOGLOBULINS NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: 4 CORRESPONDENCE ADDRESS: CARTY STREET: 126 E. LINCOLN AVENUE: P.O. BOX 2000	LT 1 PCT-US95-13795-2 STANDARD; PRT; 426 AA.  ******** *******  Sequence 2, Application PC/TUS9513795

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RESULT
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Best Local :
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 426 AA; 47234 MW; 1032622 CN;
                                                                     XXXXXX
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                                                                                                        US-08-468-540B-2
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                                                                                                                                                                                                                           215 SYLSPPSPLD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 SYLSPPSPLD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION UMBER: US/08/336,
FILING DATE: 09-NOV-1994
CILING DATE: 09-NOV-1994
CILING DATE: 09-NOV-1994
CILORISTICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 1921:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEPAX: (908) 594-6730
                                                                                                                                                                                                                                                                  Local Similarity 70.0% res 7; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATIB
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ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA ENCODING NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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STREET: 126 E
CITY: RAHWAY
STATE: NEW JE
COUNTRY: USA
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07065-0900
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PATEL, MAYUR
                                                                                                                                                                                                                                                                                    72.78;
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                                                                                                        STANDARD;
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Pred. No. 5.13e+01;
2; Mismatches 1
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No. 5.13e+01;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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                                                                                                                                                             Sequence 33, Application US/08787547
                                                                                                                                                                                                                                                                                  US-08-787-547-33
    GENERAL INFORMATION:
APPLICANT: Hedley,
APPLICANT: Curley,
APPLICANT: Langer,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application Patent No. 5858980
                                                                                                      Sequence 33, Application US/08787547 Patent No. 5783567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: No. 5858980e
UENCE 20 AA; 2160 MW; 2047 (
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APPLICANT:
APPLICANT:
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LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Jacobs, Seth H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Darby & Darby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: A1-Sabbagh, Ahmad
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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STATE: NY
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T: Hedley, Mary Lynne
T: Curley, Joanne M.
T: Langer, Robert S.
INVENTION: MICROPARTICLES FOR DELIVERY
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Miller, Ariel
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Pred. No. 6.62e+01
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TITLE OF INVENTION: OF NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS

OF NUCLEIC ACID

STREET:

225 Franklin Street

Fish & Richardson, P.C.

ADDRESSEE:

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Query Match
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Best Local (
                                                                                                     AMELIORATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION NUMBER: US.
APPLICATION NUMBER: US.
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                              SEQUENCE
                                                  SEQ ID NO:4:
                                                                                                                                                                                Patent No. 5194425
                                                                                                                                                                                                    Patent No.
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                                                                                                                                                                                                                                              XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
NAME: Fraser, Janis K.
19 REGISTRATION UNBER: 34,819
REFERENCE/DOCKET NUMBER: 0819
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5970
TELEPTAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                           FILING DATE: 21-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
                                                                                                                                                                    APPLICANT: SHARMA , SOMESH D.; LERCH, L. BERNARD; CLARK
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide JENCE 21 AA; 2312 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: (FILING DATE: 22-JAN-: CLASSIFICATION: 514 PRIOR APPLICATION DATA:
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STATE:
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TELEX: 200154
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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                                           LENGTH: 168
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                                182 AA;
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                              19707 MW; 182144 CN;
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66.7%;
71.2%;
66.7%;
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Score 47; DB 4; L
Pred. No. 6.62e+01;
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Pred. No. 6.62e+01;
3; Mismatches (
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        Length 168;
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                                                                       SEQUENCE
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14 YLATASTMD 22
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 2,053,799-0
FILING DATE: 22-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 27552-11546;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                           IMMEDIATE SOURCE:
CLONE: human marriage.
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                 TOPOLOGY:
                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 27-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                               LENGTH:
                                        Similarity
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o. 5817629
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                               Conservative
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                                                                                                                                  linear
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                                                                    n myelin basic
18459 MW; 1439
                                       71.2%;
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                             Score 47; DB 2; 1
Pred. No. 6.62e+01;
3; Mismatches (
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143992 CN;
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Sequence 5, Application US/08457245

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                                                    US-08-457-245-5
                                                                                                                                                                         SEQUENCE
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino
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GENERAL IN
                                                                                                            205 NYLNTARTLE 214
                                                                                                                                         Local Similarity
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
TITLE OF INVENTION: MOVEL PROTEIN PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASES PTP-D1
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                          SYLSTASSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: unk
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                NAME:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 22-MAY
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                                                                                                                                                                        LE TYPE: protein
345 AA; 40427 MW; 614554 CN;
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10036-2711
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                       345 amino acids
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                (212)790-9090
(212) 869-8864
                                                                                                                                                                                            unknown
                                                                                                                                          50.0%;
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22-MAY-1995
                                                   STANDARD;
                                                                                                                                                                                                     unknown
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Pred. No. 1.10e+02;
4; Mismatches 1
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5194425-3
SEQ
                                                                                                                                                                       TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL AMELIORATING AUTOIMMUNITY NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             BRIAN R.
                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5194425
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LENGTH: 384 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: ORF2 protein

DUENCE 384 AA; 41963 MW; 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Guy W.
REGISTRATION NUMBER: 30,617
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BARRY III,
APPLICANT: YUAN, Ying
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,245
APPLICATION NUMBER: 210,594 FILING DATE: 23-JUN-1988 ID NO:3:
                                                                                APPLICATION NUMBER: US/
FILING DATE: 21-JUN-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHARMA , SOMESH D.; LERCH, L. BERNARD; CLARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105-1493
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llarity 60.0%;
Conservative
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(415) 543-5043
R SEQ ID NO: 5:
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MW; 701271 CN;
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Pred. No. 1.10e+02;
3; Mismatches 1
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Best Local Similarity
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Best Local :
                                                  Matches
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CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,372
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION INVABER: US 08/136,216
FILING DATE: 13-CCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 170
SEQUENCE 184 AA; 19952 MW; 183015 CN;
                                                                                                 SEQUENCE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                         13 YLASASTMD 21
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                                                                                                                                                                                                                                          NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Nag, Bis
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                 FEATURE:
YLSTASSLD 11
                                                                                       NAME/KEY: Protein
LOCATION: 1.170
OTHER INFORMATION: /note= "Myelin basic protein"
NCE 170 AA; 18410 MW; 141752 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townse
STREET: Steuart Street Tower,
CITY: San Francisco
                                                                                                                                                                         TOPOLOGY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              ENGTH:
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ilarity 55.6%;
Conservative
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                                                  Conservative
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                                                                                                                                                                       unknown
                                                             66.7%;
55.6%;
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                                               Score 44; DB 2; I
Pred. No. 1.41e+02;
4; Mismatches C
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Tower, One Market Plaza
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Best Local 9
       Sequence 7, Application US/08222617A
                                               XXXXXX
                                                                 US-08-222-617A-7
                                                                                                                                                                                  SEQUENCE
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GENERAL INFORMATION:
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                                                                                                                                                      Local Similarity
                                                                                                                         20 SYLSTOSDIE 29
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                                                                                                       2 SYLSTASSLD 11
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 9526;
FILING DATE: 22-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for I CURRENT APPLICATION DATA: APPLICATION NUMBER: US, FILING DATE: 20-DEC-19
                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 209 AA; 23559 MW;
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Smithkline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL TITLE OF INVENTION: ATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: John E. Ho
APPLICANT: Nicola G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Smithkline
STREET: 709 Swedeland
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
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ZIP: 19406-0939
                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                       TYPE: amino acid
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ilarity 60.0%;
Conservative
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G. Wallis
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Pred. No. 1.81e+02;
2; Mismatches 2;
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AC XX
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Best Local
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                                              Sequence 6, Application US/08220151
Sequence 6, Application US/08220151 Patent No. 5529780 GENERAL INFORMATION:
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                                                                                                                                                                                   267 LSYLSGTPSL 276
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REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                            1 VSYLSTASSL 10
                                                                                                                                                                                                       Local Similarity 60.0%; es 6; Conservative
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APPLICANT: Wontenegro, E
TITLE OF INVENTION: A M
TITLE OF INVENTION: ANTI-
TITLE OF INVENTION: Quan
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/222,617A
EILING DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 822 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Penicillium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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STATE: I
COUNTRY:
                                                                                                                                                                                                                                              NAME/KEY: Domain
LOCATION: 1.822
OTHER INFORMATION: /label~ Domain III
OTHER INFORMATION: /note~ "Domain III of ACV
OTHER INFORMATION: Penicillium chrysogenum;
NCE 822 AA; 91699 MW; 3418282 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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STREET: 3(
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Garcia, Bruno
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                                                                                                                                                                                                                     65.2%;
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A Method for Influencing Beta-Lactam
Antibiotic Production and for Isolati
Quantities of ACV Synthetase
                                                                                                                                                                                                        Score 43; DB 2; Ler
Pred. No. 1.81e+02;
3; Mismatches 1;
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aa 2474-3295"
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RESULT
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Best Local :
                     AFFLICANT: LIMBACH, KEITH J.

TITLE OF INVENTION: NUCLECTIE AND AMINO ACID SEQUENCES OF TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, AND gD AND USES NUMBER OF SEQUENCES: 128

CORRESPONDENCE ADDRESS:

ADDRESSE: CURTIS, MORRIS & SAFFORD, P.C.

STREET: 530 FIFTH AVENUE, 25TH FT.
                                                                                                                                                                             Sequence 6, Application US/08413118
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                            US-08-413-118-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNIA.

ZIP: 10036
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TYCTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        862 IRYMSIVSALE 872
                                                                                                                                              Sequence 6, Application US/08413118 Patent No. 5688920
                                                                                                                                                                                                                                                                                     1 VSYLSTASSLD 11
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal JENCE 913 AA; 100233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESSEE: Curtis, Morris &
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: NY
       COUNTRY: UNITED STATES ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 25,506 REFERENCE/DOCKET NUMBER: 45
                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                              Conservative
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36.4%;
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Pred. No. 1.81e+02;
                  OF AMERICA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

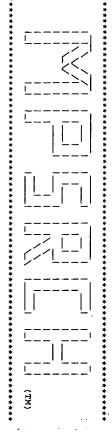
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Best Local 9
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REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
myore: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08356786
                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           862 IRYMSIVSALE 872
                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08356786 Patent No. 5877305
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein
TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VSYLSTASSLD 11
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
JENCE 913 AA; 100233 MW; 4073940 CN;
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/220,151 FILING DATE: 30-MAR-1994 ATTORNEY/AGENT INFORMATION: NAME: FROMMER, WILLIAM S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118 FILING DATE: 29-MAR-1995
                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                   COUNTRY: U:
ZIP: 02109
                                                                                                                                                           CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                USA
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36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Pred. No. 1.81e+02;
4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1255 AA
                                                                                                                                                                                                                                                         for Cancer
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Query Match
Best Local Similarity
5; Conserv
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                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           SEQUENCE
                                                                     62 LTYLPTNASL 71
                                               1 VSYLSTASSL 10
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/8:
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PItcher, Edmund R.
REGISTRATION NUMBER: 27,1
                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                      LENGTH:
                                                                                                                                          LE TYPE: protein
1255 AA; 137909 MW; 8111405 CN;
                                                                                             Conservative
                                                                                                                                                                                       1255 amino acids
                                                                                                       65.2%;
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                                                                                           Score 43; DB 2; I
Pred. No. 1.81e+02;
4; Mismatches 1
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                                                                                                                                                                                                                                                              CRP-053
                                                                                                                  Length 1255;
                                                                                            1; Indels
                                                                                            0;
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Gaps

0;

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

no on: Thu Sep 2 11:18:01 1999; MasPar time 2.14 Seconds 118.732 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Title: >US-08-599-226-3 (1-9) from US08599226.pep 66 1 QRYNRAPYX 9

Sequence:

Scoring table: PAM 150 Gap 15

77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 I:swissprot

Statistics: Mean 23.600; Variance 27.313; scale 0.864

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

7 V 7 0 10 10 10 10 10 10 10 10 10 10 10 10 1	Result
50 50 50 50 50 50 50 50 50 50 50 50 50 5	Score
81 88 88 87 77 3 3 77 77 2 77 77 2 77 77 77 77 77 77 77 77	ery tch
263 1262 263 2667 360 360 3285 1442 4442 4445 4445 4445 4447 4447 4447 4	Length
	DB 1
PRCZ_RAT PRCZ_HUMAN GNRP_MOUSE FCAR_HUMAN DCAM_SOLTU RS2_ARATH HY14_PIG TRA6_NELIME GDIA_MOUSE V1T2_DROME GDIB_HUMAN GDIB_RAT GDIIA_HUMAN GDIA_BOVIN GDIA_	ID PRC2_DROME
PROTEASOME COMPONENT C PROTEASOME COMPONENT C GUANINE NUCLEOTIDE REL IMMUNOGLOBULIN ALPHA F S-ADENOSYLMETHIONINE D 40S RIBOSOMAL PROTEIN HYPOTHALAMIC TETRADECA TRANSPOSASE FOR INSERT RAB GDP DISSOCIATION I SECRETORY PATHWAY GDP HYPOTHETICAL 77.3 KD P PROLLINE DEHYDROGENASE PROLLINE DEHYDROGENASE APOLLPOPHORIN PRECURSO HYPOXANTHINE PHOSPHORI	
4.20e-01 1.92e+00 8.13e+00 8.28e+00 8.28e+00 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01	_   <sub>10</sub>

This SWISS-PROT entry is copyright. It is produced through a collaboration

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
44	44	45	45	45	45	<b>4</b> 5	45	<b>4</b> 5	45	45	45	45	45	<b>4</b> 5	45	45	45	46	46	46	46
66.7	66.7	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	69.7	69.7	69.7	69.7
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ALBU_CHICK	Y382_METJA	POL1_BAYMG	POL1_BAYMJ	HSCA_ECOLI	LIP1_GEOCN	LIP2_GEOCN	NPRE_BACAM	MATK_HUMAN	MATK_MOUSE	PYR5_NAEGR	CG2A_DROME	MATK_RAT	TRPB_HALVO	BHMT_RAT	BHMT_HUMAN	YAFJ_ECOLI	KV1L_HUMAN	YMS5_CAEEL	EDD_PSEAE	NADA_SALTY	FARX_LYMST
SERUM ALBUMIN PRECURSO	HYPOTHETICAL PROTEIN M	GENOME POLYPROTEIN 1 [	GENOME POLYPROTEIN 1 [	CHAPERONE PROTEIN HSCA	LIPASE 1 PRECURSOR (EC	LIPASE 2 PRECURSOR (EC	BACILLOLYSIN PRECURSOR	MEGAKARYOCYTE-ASSOCIAT	MEGAKARYOCYTE-ASSOCIAT	URIDINE 5'-MONOPHOSPHA	G2/MITOTIC-SPECIFIC CY	MEGAKARYOCYTE-ASSOCIAT	TRYPTOPHAN SYNTHASE BE	BETAINE HOMOCYSTEINE	BETAINE HOMOCYSTEINE	HYPOTHETICAL 28.6 KD P	IG KAPPA CHAIN V-I REG	HYPOTHETICAL 159.2 KD	PHOSPHOGLUCONATE DEHYD	QUINOLINATE SYNTHETASE	FMRFAMIDE-RELATED NEUR
	5.22e+01	3.33e+01	3.33e+01	3.33e+01	3.33e+01	3.33e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01											

# ALIGNMENTS

01-OCT-1989 (REL. 12, CREATED) 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE) 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE) 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE) 01-OCT-1989 (REL. 13, LAST ANUTATION UPDATE) 01-OCT-1989 (REL. 13, LAST ANUTATION UPDATE) 01-OCT-1989 (REL. 13, LAST ANUTATION UPDATE) 01-OCT-1989 (REL. 12, LAST ANUTATION UPDATE) 02-OCT-1989 (REL. 12, LAST ANUTATION UPDATE) 03-OCT-1989 (REL. 12, LAST ANUTATION UPDATE) 03-OCT-1989 (REL. 12, LANUTATION UPDATE) 03-OCT-1989 (REL. 12, LANUTANUTATION UPDATE) 04-OCT-1989 (REL. 12, LANUTANUTATION UPDATE) 04-OCT-1989 (REL. 12, LANUTANUTATION UPDATE) 05-OCT-1989 (REL. 12, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLICHTLY BASIC PH. THE 35 KD SUBUNIT IS PROBABLY A REGULATORY SUBUNIT. HE PROTEASOME IS AN ANTI-SEPENDENT NON-LYSOSOMAL PROTECTION: PROTECTION: PROTECTION: PROTECTION UPDATES ON AND ALSO IN THE NUCLEUS. 1- SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE. 1- SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE. 1- SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE. 1- SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE. 1- SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE. 1- SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE. 1- SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE. 1- SUBLICATION: PROTEASOME IS COMPOSED OF AT LEAST 11 NON IDENTICAL PROTEASOME AND ALSO IN THE DECEMBENT OF THE PROTEASOME AND A HIGHL	ULT 1 PRC2_DROME STANDARD; PRT; 279 AA.
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Best Local S
Matches
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PIR; S23450; S23450.
FLYBASE; FB9N0003151; Pros35.
PROSITE: PS00388; PROTEASOME_A; 1
PFAM; PF00227; Proteasome; 1.
HSSP; P25156; 1PMA.
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PIR; !
                                                                                                                                                "The NH2-terminal residues of proteinase complex) subunits,
                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (REL. 16, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT CPROTEASOME NU CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRC2_RAT P18420;
                                                                                                                                                                          MEDLINE; 90243011.
TOKUNAGA F., ARUGA R.,
SHIMONISHI Y.;
                                                                                                                                                                                                                                                              "Molecular cloning complexes) from rat
                                                                                                                                                                                                                                                                                                    MEDLINE; 90057428.
FUJIWARA T., TANAKA K., KU
ICHIHARA A., TOKUNAGA F.,
                                                                                                                                                                                                                                                                                                                                                                                   RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
             -
                                    <del>-</del>
                                                                                                                                                                                                             TISSUE-LIVER;
                                                                                                                                                                                                                                               BIOCHEMISTRY
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                            RODENTIA;
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                                                                                                                                                                                                                        SEQUENCE OF 1-30.
                                                                                                                                                                                                                                                                                            NAKANISHI S.;
                                                                                                                                                                                                                                                                                                                                                                                                              PSMA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEASOME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                          lpha-acetylated.";
EBS LETT. 263:373-375(1990).

I- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDED
PROTEOLYTIC ACTIVITY.

PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL PATHWAY:

PROTEOLYTIC PATHWAY.

SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.

SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND ALSO IN THE NUCLEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRYNRAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRYDRRPY 128
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X62285; G8388; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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and this statement
requires a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Swiss Institute of Bioinformatics and the E Bioinformatics Institute. There are no rest-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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75.0%;
                                                                                                                                                                                                                                                                    liver:
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                                                                                                                                                                                                                                                                                CDNA
                                                                                                                                                                                     IWANAGA
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                                                                                                                                                                                                                                                                                                      KUMATORI
                                                                                                                                                                                                                                                                                                                                                                          MURIDAE;
                                                                                                                                                                                                                                                                                                                                                   PARTIAL
                                                                                                                                                                                                                                                                    primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
1; M
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                                                                                                                                                   rat
C2,
                                                                                                                                                                                                                                                                                                                                                                          VERTEBRATA;
AE; MURINAE;
                                                                                                                                                                                     s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                               proteasomes
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                                                                                                                                                                                                                                                                                                       R.,
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                   liver proteasome C3 and C8, are N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                     TANAKA K.,
                                                                                                                                                                                                                                                                    structure
                                                                                                                                                                                                                                                                                                    , SHIN S., YO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.67e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC32;
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                                                                                                                                                                                                                                                                                                                                                                           MAMMALIA;
RATTUS.
                                                                                                                                                                                                                                                                                (multicatalytic
                                                                                                                                                                                                                                                                                                 , YOSHIMURA T.,
                                                                                                                                                                                                                                                                   0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                     ICHIHARA A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                   the largest
                                                                                                                                                              (multicatalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEX SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279;
                                                                               GROUP AT
ATP-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                             C2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is in
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Best Local
                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
(PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
(PROTEASOME COMPONENT C2 (PROTEASOME COMPLEX SI
C2) (30 KD PROSOMAL PROTEIN) (PROS-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRC2_HUMAN
P25786;
                           DEMARTING G.N., ORTH K., MCCULLOUGH M.L., LE MOOMAM C.R., DAMSON P.A., SLAUGHTER C.A.; "The primary structures of four subunits of high-molecular-weight proteinase, macropain distinct but homologous.";
                                                                                                                                                                                                                                                 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A32968; SNRTC2.
PROSITE; PS00388; PROTEASOI
PFAM; PF00227; proteasome;
HSSP; P25156; 1PMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                    TAMURA T., LEE D.H., OSAKA F., F
TANAKA K., ICHIHARA A.;
"Molecular cloning and sequence
                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 91223105.
                                                                                                                                                                                                                                                                         "Two mRNAs exist for
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 93013039.
                                                                                                                                                                                                                                                                                                                                                 PSMA1 OR PSC2 OR PROS30.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEASOME; HYDROLASE; MOD_RES 1 1 1 SEQUENCE 263 AA; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ++
                 BIOCHIM.
                                                                                          SEQUENCE FROM N.A. MEDLINE; 91363412.
                                                                                                                                                          subunits of
                                                                                                                                                                                                                                                                                                                                         PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 QRYGRRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QRYNRAPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outsi European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: EXPRESSED IN ALL RAT TISSUES.

PTM: ITS C-TERMINAL EXTENSION IS PARTIALLY CLEAVED OFF
PROTEOLYSIS LEADING TO A CONVERSION OF THE PROTEASOME
LATENT INTO ITS ACTIVE FORM.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY TIA; ALSO KNOW
PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
                                                                                                                                                                                                                                              1 prosomes.";
120:235-242(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M29859; G206382; -. D90265; G220877; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
      BIOPHYS.
TION: THE
                                                                                                                                 BIOPHYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                      CATARRHINI;
                                                                                                                                                          human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
llarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEASOME_A;
pteasome; 1.
                                                                                                                                 ACTA 1089:95-102(1991)
     PROTEASOME
                 ACTA 1079:29-38(1991)
                                                                                                                                                        proteasomes
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                                                                                                                                                                                                                                                                         the:
                                                                                                                                                                                                                                                                                                                                      HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEASE; ACETYLATION.
ACETYLATION.
517 MW; 01D55620 CRC32
                                                                                                                                                                                                                                                                         COUX O., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 1;
Pred. No. 4.20e-01
SI
                                                                                                                                                                                                                                                                                                                                      VERTEBRATA;
AE; HOMO.
                                                                                                                                                        ce analysis of cDNAs (multi-catalytic pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                             FUJIWARA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
   MULTICATALYTIC
                                                                                                                                                                                                                                                                       SCHERRER K.;

D gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC32;
                                                                                                                                                                                                                                                                                                                                                    MAMMALIA; EUTHERIA;
                                                                               LEE L.W., MUNN T.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.isb-sib.ch/announce/
                                                      the
                                        the human, (proteasome),
                                                                                                                                                                                               SHIN
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   PROTEINASE COMPLEX
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Best Local S
Matches
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EMBL; D00759; G220022; -.
EMBL; X61969; G296738; -.
PIR; S15897; S15897
PIR; JC1445; JC1445.
AARHUS/GHENT-2DPAGE; 2223; IEF.
                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (REL. 23, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).
RASGRET OR CDC25MM OR GRET.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNRP_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00227; proteasome; HSSP; P25156; 1PMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                         Saccharomyces
                                                                                                                                                                                                                                                            CEN H.,
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                          MEDLINE; 92289680
MARTEGANI E., VANC
                                                                             SEQUENCE OF 791-1262 FROM N.A. STRAIN-SWISS; TISSUE-BRAIN;
                                                                                                                                                      "Isolation of multiple mouse cDNAs with coding Saccharomyces cerevisiae CDC25: identification BCr, Vav, Dbl and CDC24.";
EMBO J. 11:4007-4015(1992).
                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                          RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEASOME; HYDROLASE;
     FERRARI C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QRYGRRPY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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PROTEDLYTIC PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL PROTEDLYTIC PATHWAY:
SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND ALSO IN THE NUCLEUS.
ALTERNATIVE PRODUCTS: TWO FORMS (SHORT AND LONG) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE FOR THIS PROTEIN.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY TIA; ALSO KNOWN AS THE PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRYNRAPY
                                                                                                                                                                                                                                                               LOWY D.D.
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                                                                                                                                                                                                                                                                                       93010996.
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                                                                                                                                                                                                                                                                                                                                                                                          SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 AA;
., VANONI M., ZIPPEL R., C
STURANI E.P., ALBERGHINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
larity 75.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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M -> MOLSKYK (IN LONG FORM).

555 MW; 6CD09A93 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                          MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
0; M
                                                                                                                                                                                                                                                                                                                                                                                             VERTEBRATA; MAMMALIA; EUTHERIA;
AE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; DB 1; I
No. 4.20e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1262
                          COCCETTI
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                                                                                                                                                                                                         homology to
of a region
                             BRAMBILLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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C outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local s
Matches
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PFAM; PF00612; IQ; 1.
PFAM; PF00617; RASGEF; 1.
PFAM; PF00618; RASGEFN; 1.
PFAM; PF00621; RhoGEF; 1.
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CONFLICT
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PIR; S
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                                                                                                                                                                                                                                                                                                FCAR_HUMAN STANDARD; PRT; 287 AA. P24071; Q15728; Q15727; Q13603; Q13604; O1-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) IMMUNOGLOBULIN ALPHA FC RECEPTOR PRECURSOR (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEI W., MOSTELLER R.D., SANYAL P., GONZALES E., MCKINNEY D.,
DASGUPTA C., LI P., LIU B.X., BROEK D.;
"Identification of a mammalian gene structurally and functionally
related to the CDC25 gene of Saccharomyces cerevisiae.";
PROC. MATL. ACAD. SCI. U.S.A. 89:7100-7104(1992).
-i- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
-i- TISSUE SPECIFICITY: BRAIN.
                                                                                                                                                                                              FCAR OK LUJ.
HOMO SAPIENS (HUMAN).
CHORDATA;
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PROSITE; PS00720; GDS_CDC25;
PROSITE; PS00741; GDS_CDC24;
PROSITE; PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L20899; G388247; -. EMBL; X59868; G50358; -.
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SEQUENCE FROM N.A.
                                        MEDLINE; 91079769.
MARLISZEWSKI C..., SCH
"Expression cloning of a human Fc
"Expression cloning of a human Fc
J. EXP. MED. 172:1665-1672(1990).
                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                    PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                  ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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EMBO J. 11:2151-2157(1992).
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E.
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Pred. No. 1.92e+00;
4; Mismatches (
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021C787F CRC32;
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"ASSOCIATION OF 19A-FC receptors (Fc alpha R) with Fc epsilon RI
gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
gamma 2.";
J. IMMUNOL. 153:3228-3236(1994).

-1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS ALPHA.
MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
-1- SUBUNIT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
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VAN DIJK T.B., MORTON H.C., CALDENHOVEN E., BRACKE M
RAALJMAKERS J.A.M., LAMMERS J.W.J., KOENDERMAN L., GI
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
[5]
                                                                                                                                                            EMBL;
EMBL;
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EMBL;
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MEDLINE; 96433090.
PLEASS R.J., ANDREWS P.D., KERR M.A.
"Alternative splicing of the human :
neutrophils and eosinophils.";
BIOCHEM. J. 318:771-777(1996).
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J. IMMUNOL. 156:4442-4448/1005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE WIT T.P.M., MORTON H.C., CAPEL P.J "Structure of the gene for the human J. IMMUNOL. 155:1203-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified
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                                          PIR; JH0332; JH0332.
МІМ; 147045; -.
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A.1 BAND B-DELTA-S2 ARE PRODUCED BY ALTERNATIVE SPLICING.
A.3, B AND B-DELTA-S2 ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 2 C2-LIKE DOMAINS.
DATABASE: NAME=PROW; NOTE-CD guide CD89 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd89.htm".
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X87766; G1054737; JOINED

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        GLYCOPROTEIN;
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AND MONOCYTES;
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A Fc recept
IGA-BINDING
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Fc receptor (CD89).";
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PROTEIN;
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X MEDILINE; 95036004.

A MAD ARIF S.A., TAYLOR M.A., GEORGE L.A., BUTLER A.R., BURCH L.R.,

A DAVIES H.V., STARK M.J., KUMAR A.;

T "Characterisation of the S-adenosylmethionine decarboxylase (SAMD T gene of potato.";

PLANT MOL. BIOL. 26:327-338(1994).

L PLANT MOL. BIOL. 26:327-338(1994).

C -1- CATALTIC ACTIVITY: S-ADENOSYLMETHIONINE - (5-DEOXY-5-ADENOSY (3-AMINOPROPYL)METHYLSULFONLUM SALT + CO(2).

C -1- CATACTOR THIS ENZYME REQUIRES A PYRUVOYL GROUP FOR ITS ACTIV (3-AMINOPROPYL MOIETY REQUIRES THE ACTIVATION OF S-ADENOSYLMETHIONINE PROVIDES THE AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
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Best Local S
Matches
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SIGNAL 1
CHAIN 22
                                                                                                                                                                                                                                                                                                                      DCAM_SOLTU STANDARD; PRT; 360 AA.

Q04694;
Q04694;
Q04694;
Q01-OCT-1993 (REL. 27, CREATED)
Q1-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
S-ADEMOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETI (SAMDC) (INDUCED STOLEN TIP PROTEIN TUB13).

SAMDC) (INDUCED STOLEN TIP PROTEIN TUB13).

SAMDC OR TUB13.

SOLANUM TUBEROSUM (POTATO).
EUKARYOTA; VIRIDIPLANUTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUKARYOTA; VIRIDIPLANUTAE; STREPTOPHYTA; EUDICOTYLEDONS;
EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
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VARSPLIC
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DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                             "Expression and sequence analysis of cDNAs stages of tuberisation in different organs (Solanum tuberosum L.)."
                                                                                                                                                                                                                                                                  STRAIN-CV. RECORD; TISSUE-STOLON MEDLINE; 93081725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           TAYLOR M.A., MAD ARIF S.A., KUMAR A., PEARCE S.R., FLAVELL A.J.;
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                  ASTERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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TISSUE SPECIFICITY:
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            FROM PUTRESCINE
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POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

MISSING (IN FORM B-DELTA-S2).

MISSING (IN FORM A.3/RLA2).

MISSING (IN FORM A.2).

MISSING (IN FORM A.2).

MISSING (IN FORM A.2).

GENEROVO

EASADVARDSWSQOMCDFGLTFARTDSYCK. -> GENEROVO

EASADVARDSWSQOMCDFGLTFARTDSYCK. -> GENEROVO
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Pred. No.
2; Misma
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL).
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  EXPRESSED
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                                                                                                                                                                                                                                                                                                                  SOLANUM
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                                                                                                         decarboxylase (SAMDC)
Ä
                                                                       (5-DEOXY-5-ADENOSYL)
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AND ROOTS.
DEVELOPMENTAL

TUBER INCREASED IN SIZE.

SWELLING EARLY

OPMENTAL STAGE: TRANSCRIBED IN THE STOLON TIP DURING STAGES OF TUBERIZATION. MAXIMUM EXPRESSION WAS IN NO. 1110 TIPS FROM STAGE B, AND LEVEL DECLINED AS 1

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a collaboration -

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(See http://www.isb-sib.ch/announce/

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Best Local S
Matches
                                                                     STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X
SPRIGGS T.A., MASON T
VENTER J.C.;
                                                                                                                                                            RS2_ARATH STANDARD: PRT; 2
P49688; O22936;
01-FEB-1996 (REL. 33, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UP
15-DEC-1998 (REL. 37, LAST ANNOTATION
408 RIBOSOMAL PROTEIN S2.
RPS2 OR T11A07.6.
                                                                                                                                                                                                                                                                                                                                    CONFLICT
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     STRAIN=CV. COLUMBIA;
RAYNAL M., GRELLET F., L
SUBMITTED (OCT-1992) TO
-i- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                       ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                            SEQUENCE OF 119-285
                                                             SUBMITTED
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
                                                                                                                                                                                                                                                                       332 QKFTRTPY 339
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;; S74514;
S28047; S
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                                                                                              COLUMBIA;
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G807094; -.
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     LAUDIE M., MEYER Y., O EMBL/GENBANK/DDBJ D S TO THE S5P FAMILY O
                                                                                       KETCHUM
                                                            EMBL/GENBANK/DDBJ
                                           N.A.
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Pred.
3; M
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IMPORTANT FOR CATALYTIC A
SIMILARITY).
S -> P (IN REF. 2).
T -> S (IN REF. 2).
V -> I (IN REF. 2).
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CONVERTED TO A PYRUVOYL
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                                                                                       K.A.,
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                                                                             A.R.,
                                                                            CROSBY M.L., BRANDON A.R., ADAMS M.D., SOME
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                                                                                                                                                                               UPDATE)
                                                                                                                                                                                                                                                                                                DB 1; I
5.13e+00;
                                                                                                                                                                                                                                                                                                                                    REF.
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      ., COOKE R., DELSENY M DATA BANKS.
OF RIBOSOMAL PROTEINS
                                                           DATA BANKS
                                                                                                                                                                                                                                                                                                                                   Length 360;
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DECARBOXYLASE
                                                                                                                                                                                                                                                                                         Indels
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P01155;
21-JUL-1986
21-JUL-1986
21-JUL-1986
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SEQUENCE
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"Identification and IS1106, downstream
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PIR; A01419; NYPG14.
HSSP; P21856; IGND.
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CONFLICT 268
CONFLICT 272
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EMBL; Z17622; G
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                                                                                         STRAIN=B15
MEDLINE; 9
                                                                                                                                                                                                                                                       01-JUN-1994
TRANSPOSASE
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01-JUN-1994
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SCHALLY A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                    BACTERIA;
                                                                                                                                                                                                                                NEISSERIA
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| RYNRAPY
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Pred. No. 1.33e+01;
2; Mismatches 1
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f a novel insertion sequence.
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01-0CT-1996 (REL. 34,
01-0CT-1996 (REL. 34,
15-JUL-1998 (REL. 36,
RAB GDP DISSOCIATION 1
                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                              use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOL. CELL. BIOL. 14:3459-3468(1994).

-!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM T SUBSEQUENT BINDING OF GTP TO THEM.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-!- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, LOWER I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHISHEVA A., SUDHOF T.C., CZECH M.P.;
"Cloning, characterization, and expression of a nove dissociation inhibitor isoform from skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;

EUKARYOTA; MCTIBOCNATHI: MURIDAE; MURINAE;
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2 RYNRAPY
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SEQUENCE 288
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                                                                                                                                              PF00996; GDI; P21856; 1GND.
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                                                                                                                     ACTIVATION.
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ELEMENT; TRANSPOSITION; DNA-BINDING;
88 AA; 32758 MW; 068FF8FA CRC32;
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INVOLVED IN THE TRANSPOSITION OF THE INSERTION
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34, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
36, LAST ANNOTATION (RAB GDI
71.2%;
57.1%;
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  DB 1; I
1.33e+01;
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Matches 6; Conser
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P50395;
01-OCT-1996 (REL.
01-OCT-1996 (REL.
15-JUL-1998 (REL.
                                                                                 01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI GDI2 OR RABGDIB.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. MOL. BIOL. 164:481-492(1983).

-!- FUNCTION: VITELLOGENIN IS THE MAJOR YOLK PROTEIN OF EGGS WHERE IT IS USED AS A FOOD SOURCE DURING EMBRYOCENESIS.
-!- TISSUE SPECIFICITY: SYNTHESIZED IN THE FAT BODY AND OVARIAN FOLLICLE CELLS AND ACCUMULATE IN THE OOCYTE.
-!- INDUCTION: IN MALES BY BETA-ECDYSONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIT2_DROME P02844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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PIR; A03333; VJFF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HI
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
VITELLOGENIN II PRECURSOR (YOLK PROTEIN 2).
  TISSUE-BRAIN
                                                                        PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
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PFAM; PF00151; lipase; 1.
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                      SEQUENCE FROM
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                                                                     CATARRHINI;
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442 AA;
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larity 75.0%;
Conservative
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                                                                        HOMINIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 1;
Pred. No. 1.33e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VITELLOGENIN II.
; A433872E CRC32;
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                                                                                      VERTEBRATA; MAMMALIA; EUTHERIA;
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Best Local
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P50399;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                        MEDLINE; 95298038.

ARAKI K., NAKANISHI H., HIRANO H., KATO M., SASAKI T., TAKAI YARAKI K., NAKANISHI H., HIRANO H., KATO M., SASAKI T., TAKAI YARAKI K., NAKANISHI H., HIRANO H., KATO M., SASAKI T., TAKAI YARAKI K., NAKANISHI H., HIRANO F. RAB GDI beta from rat bi BIOCHEM. BIOPHYS. RES. COMMUN. 211:296-305(1995).

-!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, SUBSEQUENT BINDING OF GTP TO THEM.

-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
                                                                                                                                                                                      J. BIOL.
[2]
                                                                                                                                                                                               NISHIMURA N., NAKAMURA H., TAKAI Y., SANO K.;
"Molecular cloning and characterization of two
rat brain: brain-specific and ubiquitous types.
J. BIOL. CHEM. 269:14191-14198(1994).
                                                                                                                                                                                                                                                                                                                                                                          RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI BETA) (GDI-2).
GDI2 OR RABGDIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACHNER D., SEDLACEK Z., KORN B., HAMEISTER H., POUSTKA A.; "Expression patterns of two human genes coding for different dissociation inhibitors (GDIs), extremely conserved proteins in cellular transport."; HUM. MOL. GENET. 4:701-708(1995).
                                                                                                                                                                                                                                                                                                                                             RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D13988; G285975; MIM; 600767; -.
                                                                                                                                                                      SEQUENCE OF 30-54 AND 58-74, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                     MEDLINE; 94245743
                                                                                                                                                                                                                                                                                                                                   RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDIB_RAT
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SUBMITTED (APR-1993) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 RYGKSPY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RYNRAPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS BY INHIBITING THE DISSOCIATION SUBSEQUENT BINDING OF GTP TO THEM.
TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . MOL. GENET. 4:701-708(1995). FUNCTION: REGULATES THE GDP/GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF
                SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INHIBITOR.
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P21856; 1GND.
SE ACTIVATION.
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                                                                                                                                                                                                                                                                                                                              SCIUROGNATHI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                 BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.2%;
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O EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                              MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 1; Pred. No. 1.33e+01 2; Mismatches
                                                                                                                                                                                                                                                                                                                            VERTEBRATA;
AE; MURINAE;
              TCD/MRS6 FAMILY OF
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RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 445;
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              GDP DISSOCIATION
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                                                                                                                                       TAKAI Y.;
                                                                                                                                                                                                                                   species
                                                                                                                       rat brain.";
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Query Match
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Matches 4; Conser

Conservative

71.2%; 57.1%;

Score 47; DB 1; Pred. No. 1.33e+01 2; Mismatches

Length 445;

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218 RYGKSPY

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Matches
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P50397;
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01-OCT-1996 (REL. 34, LAST SHOUENCE UF
15-JUL-1998 (REL. 36, LAST ANNOTATION
RAB GDP DISSOCIATION INHIBITOR BETA (R
GDI2 OR RABGDIB.
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X74401; G396433; -. PFAM; PF00996; GDI; 1. HSSP; P21856; IGND. GTPASE ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dissociation inhibitor isoform from skeletal muscle MOL. CELL. BIOL. 14:3459-3468(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHISHEVA A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS
EUKARYOTA; MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                             HSSP;
                                                                                                                                          EMBL;
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tes 4; Conser
3L; U07951; G1486480; A
N; MGI:99845; GDI2.
AM; PPG09996; GDI; 1.
SP; F21856; IGND.
PASE ACTIVATION.
PUENCE 445 AA; 50653
                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL. BIOL. 14:3459-3468(1994).
FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, SUBSEQUENT BINDING OF GTP TO THEM.
SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATED.
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57.1%;
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THI; MURIDAE; MURINAE; MUS.
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Pred. No. 1.33e+01;
2; Mismatches 1
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DEFINITION STANDARD;

C P31150; P50394;

C P31150; P50394;

T 01-UL-1993 (REL. 26, CREATED)

DT 01-CCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE RAB GDP DISSOCIATION INHIBITOR ALPHA (RAB GDI ALF

GN GDI1 OR RABGDIA OR XAP4.

OS HOMO SAPIENS (HUMAN).

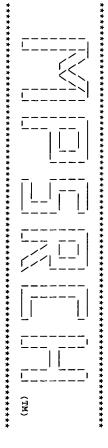
OS HOMO SAPIENS (HUMAN).

THRARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMAJ
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                                                                                                                                                                                                                                                                                                                                   BACHNER D., SEDLACEK Z., KORN B., HAMEISTER H., POUSTKA A.;
"Expression patterns of two human genes coding for different rab GDP-dissociation inhibitors (GDIs), extremely conserved proteins involved in cellular transport.";
HUM. MOL. GENET. 4:701-708(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RASMUSSEN H.H., VAN DAMME J., PUYPE M., GESS VANDEKERCKHOVE J.;
"Microsequences of 145 proteins recorded in protein database of normal human epidermal benefictrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZUO L., HEINER C.,
D'URSO M.;
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NISHIMURA N., GOJI J., NAKAMURA H., ORITA S., TAKAI Y., SA "Cloning of a brain-type isoform of human Rab GDI and its in human neuroblastoma cell lines and tumor specimens."; CANCER RES. 55:5445-5450(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 95152170.
SEDLACEK Z., KONECKI D.S.,
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY. MEDLINE; 95359978.
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                                                                                                                                                                                                    . MOL. GENET. 4:701-708(1995).
FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF PROTEINS BY INHIBITING THE JISSOCIATION OF GDP FROM T SUBSEQUENT BINDING OF GTP TO THEM.
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
TISSUE SPECIFICITY: BRAIN; PREDOMINANT IN NEURAL AND
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SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermal keratinocytes.";
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

In on: Thu Sep 2 11:19:02 1999; MasPar time 1.35 Seconds 67.852 Million cell updates/seconds

Title: >US-08-599-226-3 Description: (1-9) from US08599226.pep Perfect Score: 66

Sequence: 1 QRYNRAPYX 9
Scoring table: PAM 150
Gap 15

Searched: 106580 segs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 15.499; Variance 48.116; scale 0.322

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
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APPLICANT: MALIISZEWSKI, CHARLES R.

TITLE OF INVENTION: DNA ENCOGING IGA FC RECEPTORS // NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                  US-07-971-092-2
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                                                                                                                                                                                          Sequence 2, Application US/07971092
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                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:
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                                                                                                                                                     GENERAL INFORMATION:
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Local Similarity 75.0%;
hes 6; Conservative
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                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Tmm...
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APPLICATION NUMBER: US/07/548,059
FILING DATE: 05-JUL-1990
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human
JENCE 269 AA; 30227 MW; 341084 CN;
                                                                                                                                 APPLICANT: Maliszewski, Charles R. TITLE OF INVENTION: Hulga Fc Receptor
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                                                                STATE: W
                                                                                   STREET: 51 Uni
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        SOFTWARE:
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CE 311 AA; 34908 MW; 558002 CN;
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 APPLICATION DATA:
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                                                                                              51 University
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                                                                  USA
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         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                  STANDARD;
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Pred. No.
2; Misma
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Pred. No. 1.41e+01;
0; Mismatches 2;
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Best Local S
Matches
                                                                    TELEFAX: (212) 869-8864,
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-604-989A-3
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08604989A
Patent NO. 5834208
GENERAL INFORMATION:
APPLICANT: Sakano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 WYNRSPY 202
                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARR: FASTSEO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,98
FILING DATE: FEBRUARY 23, 1996
CLASSIFICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: Charles E. Miller
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 1920-02
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34693
REFERENCE/DOCKET NUMBER: 21
INFORMATION FOR SEQ ID NO: 2:
                 LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human
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LENGTH: 287 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sakano, S.
TITLE OF INVENTION: NO
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: protein
JENCE 287 AA; 32265 MW; 435416 CN.
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Amer.
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          STRAIN:
246 AA; 27425 MW; 326654 CN;
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llarity 71.4%;
Conservative
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Pred. No. 3.83e+01;
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Best Local Similarity 83.3%;
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Best Local Similarity
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                                                                                                                                            SEQUENCE
                   PCT-US95-05008-2
                                                                        379 YGRAPY 384
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                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,98
FILING DATE: February 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles E Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                            TELEFAX: (212) 869-8864/9:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              MOLECULE TYPE: FORIGINAL SOURCE: DORGANISM: huma
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
                                                                                                                                                       STRAIN:
                                                                                                                                                                                                                   LENGTH:
                                                                                                                                           466 AA; 51898 MW; 1114727 CN;
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                                                                                                                                                                                                        amino acid
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Pred. No. 1.30e+02;
0; Mismatches 1
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Pred. No. 1.30e+02;
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                                                                                                                       Length 466;
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                Sequence 5, Application US/08604989A
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Local Similarity 83.3%;
les 5; Conserva+4...
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
                                                                                                                                                                                                                                                                           3 YNRAPY 8
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: JENCE 507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/05008 FILING DATE: 24-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
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Hofgarten Str. 2
Munchen 80539
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515 Galveston Drive
Redwood City, California
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
56469 MW; 1316735 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 3; Length 507; Pred. No. 1.30e+02; 0; Mismatches 1; Indels
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Query Match
Best Local S
Matches
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REFERENCE/DOCKET NUMBER: 1920-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
TYPOR: amino acids
                                                                                                                                                          Sequence 12, Application US/08724194
                                                                                                                                                                                                                        US-08-724-194-12
                                                                                                                                                                                                                                                                                                                                                STRAIN: UT-7
SEQUENCE 507 AA; 56491 MW; 1317560 CN;
                                                                                                                            Sequence 12, Application US/08724194 Patent No. 5824875
                                                                                                                                                                                                                                                                            420 YGRAPY 425
                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08604989A
Patent No. 5834208
                                                                                                      GENERAL INFORMATION:
APPLICANT: RANU, RAJINDER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 3 YNRAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/604. FILING DATE: February 23, 199 CLASSIFICATION: 435
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sakano, S. TITLE OF INVENTION: N. NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
ZIP: 100
           STREET: 315 WEST O CITY: FORT COLLINS STATE: CO
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charles E. Miller
                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                   68.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  February 23, 1996
                                                                                                                                                                                                                        STANDARD;
                                                                       ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVEL
IN GERANIUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO.
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Pred. No. 1.30e+02;
0; Mismatches 1
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Best Local :
                                                                                                                                                                                                                                                                 Patent No. 30307...
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Vuan
APPLICANT: Chang, Yuan
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Unique Ass
TITLE OF INVENTION: Virus Sequences: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO. LITTE
                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08343101A
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-343-101A-20
                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08343101A Patent No. 5830759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (970) 224-3:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| ||
3 YNRAPY 8
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                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-A
                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
         TELECOMMUNICATION INFORMATION: TELEPHONE: 212-278-0400
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 33 AA; 3822 MW; 5035 CN;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                      COUNTRY: U. ZIP: 10036
                                                                                                                                                                                                              CITY: New York
STATE: New Yorl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                         FILING DATE:
                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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D NO: 12:
                                                                                                     US/08/343,101A
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Pred. No. 1.65e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                  Sequences
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equences And Uses Thereof
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS

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Best Local Similarity 71.4%;
Matches 5; Conservative
Query Match
Best Local Similarity
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US-07-989-991A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2,
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                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 RYNRGLY 125
                                                                                     REFERENCE/DOCKET NUMBER: BT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 861-6240
TELEFAX: 617 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RYNRAPY 8
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIO Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,991A
FILING DATE: 07-DEC-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thireos, George
APPLICANT: Kafetzopoulos, Dimitris
TITLE OF INVENTION: DNA ENCODING CHITIN DEACETYLASE
NUMBER OF SEQUENCES: 2
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,
                                 MOLECULE TYPE: protein
JENCE 400 AA; 43857 MW; 860821 CN;
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: N
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                                                      LENGTH: 4
TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..218
OTHER INFORMATION:
NCE 218 AA; 24345 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Peptide LOCATION: 1..218
                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/07989991A
                                                     I: 400 amino acids
amino acid

GY: linear
                                                                                                                                                                                                                                                                                                                        Lexington
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                                                                                                                                                                                                                                                                                                    USA
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Pred. No. 1.65e+02;
1; Mismatches 1
 Score 44; DB 1; I
Pred. No. 1.65e+02;
                                                                                                                                                        22,592
                                                                                                                                                                                                                                                                                                                                              Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253377 CN
                                                                                                                                             BTT91-01A
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           Length 400
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                                                Query Match
Best Local :
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                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08748485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 581/~~.
Patent No. 581/~..
PawerAL INFORMATION:
An-You
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Appitus
+ No. 5817480
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                    343 DRYYREPF 350
                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RYNRAPY 8
  1 QRYNRAPY 8
                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 96,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Goli, Surya K.
APPLICANT: Murry, Lynn E.
                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                               LIBRARY: COMC-
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: UNFILING DATE: Herewith
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                  TOPOLOGY:
                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                      4;
                                                                           454 AA;
                                      66.7%;
llarity 50.0%;
Conservative
                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                               Consensus
                                                                                                                   linear
                                                                            50589 MW; 1146364 CN;
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                                                                                                                          single
                                                                                                                                                                                                                                                                                                      US/08/748,485
                                                Score 44; DB 2; L
Pred. No. 1.65e+02;
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                                       Mismatches
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                                                       Length 454;
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RESULT

US-08-467-568-2

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RESULT
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Matches
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 529 AA; 58358 MW; 1481658 CN;
                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                           Sequence 2, Application PC/TUS9409051
                                                                                                                                                         XXXXXX
                                                                                                                                                                              PCT-US94-09051-2
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                                                                                                                                                                                                                                             342 DRYYREPF 349
                                                                                      Sequence 2, Application PC/TUS9409051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application
                            GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Adrenergic Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                        1 QRYNRAPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ADRENERGIC RECEPTOR NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6 Becke
CITY: Roseland
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ferraro, Gregory REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 06-JUN
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART 6 OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPPET,
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                                                                                                                                                                                                                                                                              50.0%;
                                                                                                                                                                              STANDARD;
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Pred. No. 1.65e+02;
2; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 PCT-US95-10194-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                342 DRYYREPF 349
                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9510194 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE SEARCH SEQ ANINO ACID
                                                                                                                                                                                                                                                                                                                                                                            1 QRYNRAPY 8
                                                                                                                                                                                     APPLICANT: The Trust
APPLICANT: City
TITLE OF INVENTION:
TITLE OF INVENTION:
                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                       COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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MOLECULE TYPE: PROTEIN
MOLECULE TYPE: PROTEIN
JENCE 529 AA; 58358 MW; 1481658 CN;
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MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: Submit CLASSIFICATION:
                                                                                                                     CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACIDS
FILING DATE:
CLASSIFICATION:
                                                                                                                                            STREET:
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NEW JERSEY
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                                                                                                                     New York
                                                                                                                                          1185 Avenue of the Americas
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                                                                                                                                                                                                                   The Trustees of Columbia University in the City of New York
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                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                     UNIQUE ASSOCIATED KAPOSI'S SEQUENCES AND USES THEREOF
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                     PCT/US95/10194
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 3;
Pred. No. 1.65e+(
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-C-PCT/JPW/MSC
TELECOMMUNICATION INFORMATION:

ATTORNEY/AGENT INFORMATION:

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Best Local Similarity 71.4%;
Matches 5; Conservative
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08420235B Patent No. 5801042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RYNRAPY 8
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MOLECULE TYPE: protein
JENCE 1376 AA; 153401 MW; 9818578 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1376 amino acids
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                MOLECULE
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chang, Yuan APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 11
                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                            APPLICATION NUMBER:
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                     1376 AA; 153401 MW; 9818578 CN;
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                                                    amino acid
                                 TYPE:
                                                              1376 amino acids
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1185 Avenue of the Americas
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(212) 391-0525
                                          linear
 66.7%;
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Score 44; DB 2;
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Pred. No. 1.65e+02;
1; Mismatches 1
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Length 1376;
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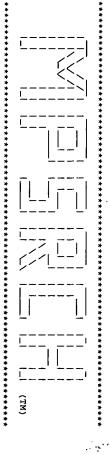
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В
                         Best Local Similarity 71.4%;
Matches 5; Conservative
1277 RYNRGLY 1283
                         Pred. No. 1.65e+02;
1; Mismatches 1;
                         Indels
                         0;
                        Gaps
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Search completed: Thu Sep Job time: 8 secs. 2 11:19:10 1999 δÃ

2 RYNRAPY 8

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp un on: protein - protein database search, using Smith-Waterman algorithm

Thu Sep 2 11:17:30 1999; MasPar time 3.08 Seconds 116.921 Million cell updates/sec

bular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-599-226-3 (1-9) from USU8599226.pep 66 1 QRYNRAPYX 9

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Statistics: Mean 22.973; Variance 30.279; scale 0.759

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Query	Length	DB	IĐ	Description	Pred. No.
1	57	86.4	279	1	SNFF5K	multicatalytic endope	.45e-
N	54		263	ب	н	ticatalytic	
ω	54		269	N	JC1445		٠
4	53		790	2	S77032	-type transp	2.27e+00
տ	52		321	N	B71854	II DNA modific	
σ	51		1260	2	S28407	ine nuc	5.63e+00
7	50		239	N	G02630	×	
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9	50		521	N	I39956	tral proteinas	
10	49		360	N	S52662	_	
11	49		360	N	S28047	TUB13 protein - potat	•
12	48		367	N	S49009	tein 2	
13	48		370	N	S49008		•
14	48		534	N	S71800	transcription factor	•
15	48		1032	N	S74487	ס	•
16	47	71.2	14	_	NYPG14		3.24e+01
17	47		288	N	S22628	hypothetical protein	'n
18	47		323	N	C56024	4	
19	47		355	N	S76940	hypothetical protein	3.24e+01
20	47	:	440	ν	F70792		
21	47	:	442	ᆫ	VJFF2		
22	47	71.2	445	N	C56956	tion	
23	47	71.2	445	N	B54091	rab GDP dissociation	3.24e+01

45	44	43	42	41	40	39	ა 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24
45	45	46	46	46	46	46	46	47	47	47	47	47	47	47	47	47	47	47	47	47	47
68.2	68.2	69.7	69.7	69.7	69.7	69.7	69.7	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2
544	527	1409	613	419	365	182	106	1320	1320	722	689	541	520	515	451	448	447	447	447	447	445
N	N	N	N	ω	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
S41093	A49865	S41028	S55615	JE0389	C37753	S45202	G02071	D64843	S66279	C71411	S45901	S01957	B71143	T03070	S44446	S36746	B56024	137082	A35652	A54091	A56024
triacylglycerol lipas	protein-tyrosine kina	hypothetical protein	thymidine kinase (EC	catabolite repressor	quinolinate synthase	hypoxanthine phosphor	helicase - human (fra	proline dehydrogenase	proline dehydrogenase	hypothetical protein	probable membrane pro			hypothetical protein	GDP dissociation inhi	GDP dissociation inhi	GDP dissociation inhi	ĩ	smg p25A regulatory p	rab GDP dissociation	GDP dissociation inhi
7.47e+01	7.47e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01	3.24e+01

# ALIGNMENTS

Query Match	#gene pros-15 ##cross-references #map_position 89F-90A #introns 1/3; 21: CLASSIFICATION #superfi KEYWORDS hydrola: SUMMARY #length	##molecule_type mRNA ##residues 1.27 ##cross-references E #accession A38761 ##molecule_type prot ##residues 4.18 GENETICS	#authors #journal #title #cross-refere #accession	#cross-references MUID #accession \$23450 #accession type DNA ##molecule_type DNA ##residues 1-2 ##cross-references ##experimental_sour REFERENCE \$05507	#authors #journal #title	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS BEEDESUCE
86.4%; Score 57; DB 1; Length 279;	PROS-35 ferences FlyBase:FBgn0003151 89F-90A 1/3; 211/3 #superfamily multicatalytic endopeptidase complex chain C9 hydrolase; phosphoprotein; proteinase #length 279 #molecular-weight 31058 #checksum 365	##molecule_type mRNA ##rcsidues 1-279 ##label HAA ##rcoss-references EMBL:X15497; NID:g8381; PID:g8382 cession A38761 ##molecule_type protein ##residues 4-18;194-206 ##label HAA2	#AUTHORS HARS, C.; PESOIG-HURT, B.; MUITHAUP, G.; Beyreuther, K.; #journal EMBO J. (1999) 8:2373-2379 #title The PROS-35 gene encodes the 35 kd protein subunit of #cross-references MUID:90005444 #accession S05507	OS-Dm35. :92249308 79 ##label FREN FEMBL:X62285; NID:g8387; PID:g8388 Ce strain Canton S	Prentzel, S.; Troxell, M.; Haass, C.; Pesold-Hurt, B.; Glaetzer, K.H.; Kloetzel, P.M.  Eur. J. Biochem. (1992) 205:1043-1051  Molecular characterization of the genomic regions of the Drosophila alpha-type subunit proteasome genes PROS-Dm28.1	SNFF5K #type complete multicatalytic endopeptidase complex (EC 3.4.99.46) 35K chain - fruit fly (Drosophila melanogaster) 19S cylinder particle 35K chain; multicatalytic proteinase 35K chain; prosome 35K chain; proteasome 35K chain #formal_name Drosophila melanogaster 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Sep-1997 23450; S05507; A38761

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ACCESSIONS
REFERENCE
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Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Tokunaga, F.; Aruga, R.; Iwanaga, S.; Tanaka, K.; I
#journal FEBS Lett. (1990) 263:373-375
#title The NH2-terminal residues of rat liver proteasome (multicatalytic proteinase complex) subunits, C2, C8, are N-alpha-acetylated.
#cross-references MUID:90243011
#accession S09741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Fujiwara, T.; Tanaka, K.; Kumatori, A.; Shin, S.; Yoshimuz
T.; Ichihara, A.; Tokunaga, F.; Aruga, R.; Iwanaga, S.;
Kakizuka, A.; Nakanishi, S.
#journal Biochemistry (1989) 28:7332-7340
#title Molecular cloning of cDNA for proteasomes (multicatalytic proteinase complexes) from rat liver: primary structure the largest component (C2).
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##molecule_type protein

1-30 ##label TOK
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cession A38799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 QRYDRRPY 128
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                                                                                                                                                                                                                           1
                                                                                                                                                                                                                                                                                                             Local Similarity 75.0% nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                         JC1445 #type complete
multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2,
long splice form - human
macropain nu chain; multicatalytic endopeptidase complex HC2
chain; multicatalytic endopeptidase complex nu chain;
multicatalytic proteinase chain C2; prosome 30-3K chain;
multicatalytic proteinase chain C2; prosome 30-3K chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A32968
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#formal_name Rattus norvegicus #common_name Norway rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *superfamily multicatalytic endopeptidase complex acetylated amino end; hydrolase; proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNRTC2 #type complete multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2
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31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                             #length 263
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proteasome alpha 1 subunit; proteasome chain C2; proteasome
nu chain
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2-25;42-58;63-74,'X',76-79,'X',81;116-135;190-203;
218-226,'XX',229,'X',231;244-246,'X',248-262 ##label
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#modified_site acetylated amino er
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                                                                                                                                                                                                                                                                                                                              81.8%;
75.0%;
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Pred. No. 1.43e+00;
0; Mismatches 2;
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1; Mismatches 1;
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Iwanaga, S.;
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Query Match
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#Citle Human protessome subunits by partial sequencing.

#cross-references MUID:95110324

#accession PC2321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors DeMartino, G.N.; Orth, K.; McCullough, M.L.; Lee, L.W.; Munn, T.Z.; Moomaw, C.R.; Dawson, P.A.; Slaughter, C.A.
#journal Blochim. Blophys. Acta (1991) 1079:29-38
#title The primary structures of four subunits of the human, high-molecular-weight proteinase, macropain (proteasome), are distinct but homologous.
#cross-references_MUID:91363412
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10-40;46-61;68-75;89-95;103-128;132-148;164-168;176-195;
##residues 203-223;225-267 ##label DE2
                                                                                                                                                                                                                                                                                                                                                                                       ##mollecule_type protein
##residues 69-88 ##label KRI
##experimental_source placenta
##experimental_source consists of subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references GB:X61969; NID:g296737; PID:g296738
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Biochim. Biophys. Acta (1991) 1089:95-102
Molecular cloning and sequence analysis of cDNAs for fimalor subunits of human proteasomes (multi-catalytic
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Gene (1992) 120:235-242
Two mRNAs exist for the
of human prosomes.
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                                             #length
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                                                                                                            #product multicatalytic endopeptidase complex chain C2, long splice form #status predicted #label MATI\
product multicatalytic endopeptidase complex chain C2, short splice form #status predicted #label MATS\
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                                        #molecular-weight 30239 #checksum 5946
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Best Local Similarity 62.5%;
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DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC6803. II. Sequence and assignment
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ABC-type transport protein sll0778 - Synechocystis sp.
(strain PCC 6803)
protein sll0778
#formal_name Synechocystis sp.
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type II DNA modification enzyme (methyltransferase)
Helicobacter pylori (strain J99)
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Library, June 1996
#superfamily ATP-binding cassette homology
P-loop; transport protein
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                   In, R.A., Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D. Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.
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#region nucleotide-binding motif A (P-loop)
pth 790 #molecular-weight 87656 #checksum 7314
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sequence comparison of two unrelated isolates of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53; DB 2; Length 790; Pred. No. 2.27e+00;
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                                                                                                                                            Brown, E.D.;
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                                    1021-1257
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#accession B71854
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                                                                                                                                                                                  ##status preliminary
##molecule_type nucleic acid
##residues 1029-1030,'D',1032-1224 ##label
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martegani, E.; Vanoni, M.; Zippel, R.; Coccetti, P.;
Brambilla, R.; Ferrari, C.; Sturani, E.; Alberghina, L.
EMBO J. (1992) 11:2151-2157
Cloning by functional complementation of a mouse cDNA
encoding a homologue of CDC25, a Saccharomyces cerevisiae
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S22693
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#length
                                                                                          sequence extracted from NCBI backbone (NCBIN:111101, NCBIP:111102)
#superfamily CDC25-type guanine nucleotide exchange activator homology; CDC24 homology; pleckstrin repeat homology
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#domain CDC25-type guanine nucleotide exchange activator
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75.0%;
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#molecular-weight 143900 #checksum 9725
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Pred. No. 3.
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3.58e+00;
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##cross-references GDB:127543; OMIM:147045

#map_position 19413.2-19413.4

#introns 12/1; 24/1; 121/1; 217/1

KEYWORDS 9lycoprotein; immunoglobulin re
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Best Local
                                                                                                                                                                                                                             #authors
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#journal J. Exp. Med. (1990) 172:1665-1672

#title Expression cloning of a human Fc receptor for 
#cross references MUID:91079769

#accession JH0332
                                                                                                                                                           #cross-references MUID:95363085
#accession I37224
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                                                                                                                                                                                                                                                    **residues 1-287 ##label MAL
##cross-references GB:X54150; NID:g31329; PID:g31330
##experimental_source myeloid cell liver v937
NCE 137224
                                                                                                      ##status
#molecule_type DNA
##nolecule_type DNA
1-287 ##label
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#length 239 #molecul
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##residues 1-23
                                                                                               ##cross-references EMBL:X87767;
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JAA (FC Receptor, myeloid cell (CD89) precursor
myeloid glycoprotein (D89
#formal_name Homo sapiens *common_name man
12-Feb-1993 *sequence_revision 12-Feb-1993 *text_
                                                                                                                                                                                           de Wit, T.P.; Morton, H.C.; Capel, P.J.; van de Winkel, J.G
J. Immunol. (1995) 155:1203-1209
Structure of the gene for the human myeloid IgA Fc receptor
(CD89).
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Raaijmakers, J.A.M.; Lammers, J.
submitted to the EMBL Data Library, April 1996
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larity 71.4%;
Conservative
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FcalphaRb - human
#formal_name Homo sapiens #common_name man
21-Dec-1996 #sequence_revision 06-Jun-1997
17-Jul-1998
                                                                   GDB:FCAR; CD89
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Pred. No. 8.80e+00;
2; Mismatches 0;
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i. No. 5.63e+00;
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lar-weight 26996 #checksum
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Best Local Similarity
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                                                                                            ##status preliminary
##molecule_type DNA
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##residues 1-5
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                                                                                ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-521 ##label
##cross-references GB:M36723;
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                  Similarity
 4.
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Manabe, K.; Furutani, Y.
J. Biotechnol. (1985) 2:75-85
The nucleotide sequence and some properties of the
protease gene of Bacillus amyloliquefaciens.
139956
                                                                                                                                                       Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.; Burch, L.R.; Davies, H.V.; Stark, M.J.R.; Kumar, A. Plant Mol. Biol. (1994) 26:327-338

Characterisation of the S-adenosylmethionine decarboxylase
74.2%;
llarity 50.0%;
Conservative
                                                              #length
                                                                                                                             S52662
                                                                                                                                                                                                                                                                    S-adenosylmethionine decarboxylase (SAMDC) - potato #formal_name Solanum tuberosum #common_name potato 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #superfamily thermolysin
hydrolase; metalloproteinase
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neutral proteinase (EC 3.4.24.-) - Bacillus amyloliquefe
#formal_name Bacillus amyloliquefaciens
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
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                                                                                                                                          SAMDC) gene of potato.
                                                              1-360 ##label ARI
|th 360 #molecula
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62.5%;
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                                                              #molecular-weight 39724 #checksum
Score 49; DB 2;
Pred. No. 1.37e+01
3; Mismatches
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Pred. No. 8.80e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 2; I
Pred. No. 8.80e+00;
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NID:g143352; PID:g143353
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Best Local Similarity
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Best Local Similarity 83.3%;
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##cross references EMBL:X74316; NID:g511161;
FFICATION #superfamily unassigned fork head
DNA-binding domain homology
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                                                                                             337 YNRSPY 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             potato plant (Solanum tuberosum L.). $28047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie, L.A.; Pearce, S.R.; Flavell, A.J. Plant Mol. Biol. (1992) 20:641-651
Expression and sequence analysis of cDNAs induced during the early stages of tuberisation in different organs of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUB13 protein - potato
#formal_name Solanum tuberosum #common_name potato
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
09-Sep-1997
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S49008
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Spatial and temporal transcription patterns of the forkhead related XFD-2/XFD-2' genes in Xenopus laevis embryos.
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S49008
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                                                                                                                                                                                                                                                                                                                         preliminary
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50.0%;
#type complete
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Pred. No. 1.37e+01
3; Mismatches
                                                                                                                             Pred.
                                                                                                                                          Score 48; DB 2; I
Pred. No. 2.11e+01;
                                                                                                                             Mismatches
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                                                                                                                                                         DB 2; Length 367;
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                                                                                                                           Indels
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#cross-references_MIID:94257528
                                                                                                                                                                                            #accession
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                     117-209
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##residner
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##molecule_type mRNA
##residues 118-228 ##label KNO
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                                                                                                               ##cross-references EMBL:U70980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knochel, S.; Lef, J.; Clement, J.; Klocke, B.; Hille, S.; Koster, M.; Knochel, W.
Mech. Dev. (1992) 38:157-165
Activin A induced expression of a fork head related gene in posterior chordamesoderm (notochord) of Xenopus laevis
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#formal_name Xenopus laevis #common_name African clawed

07-May-1995 #sequence_revision 21-Jul-1995 #text_change

17-Mar-1999

349008; B56556
                                                                                                                                                                                                                             Chen, X.; Rubock, M.J.; Whitman, M. Nature (1996) 383:691-696
A transcriptional partner for MAD p signalling.
                                                                                                                                                                                                                                                                                                                                                           transcription factor FAST-1 - African clawed frog (fragment) forkhead activin signal transducer 1 formal_name Xenopus laevis #common_name African clawed frog 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change
                                                                          #superfamily unassigned fork head proteins;
   DNA-binding domain homology
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#domain
#length 534
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larity 83.3%;
Conservative
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                                                       DNA binding;
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fork head DNA-binding #checksum 6119
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                                                        transcription factor
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Pred. No. 2.11e+01;
1; Mismatches 0;
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                   domain
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                   homology #label FHD
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Query Match

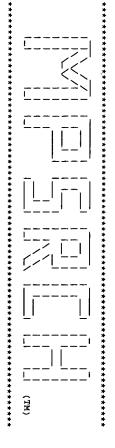
72.78;

Score 48;

DB 2;

Length 534;

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GENETICS
#Start_codon
SUMMARY
                                                                                                                                                                                                                                                                                  ACCESSIONS
REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                  RESULT
ENTRY
TITLE
                                                                                                                                                                                                                                                                                                                    DATE
Search completed: Thu Sep
Job time : 14 secs.
                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                 Query Match 72.7%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                               #variety
                                                                                                       708 REDRDPY 714
                                                                                                                                                                                                                                                                                                                                                                                                     113 HRYYKPPY 120
                                  2 RYNRAPY 8
                                                                                                                                                                                                                                                                                                                                                                                           1 QRYNRAPY 8
                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                       GTG
#length 1032 #molecular-weight 117162 #checksum
                                                                                                                                                                                                                                                                                         #formal_name Synechocystis sp.
PCC 6803
                                                                                                                                                                                                                                                                                                                                           S74487 #type complete
hypothetical protein sll1060 - Synechocystis sp. (strain PCC
6803)
          2 11:17:44 1999
                                                               Score 48; DB 2; Length 1032
Pred. No. 2.11e+01;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.11e+01;
3; Mismatches 1;
                                                                                 Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                 9339
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                                                                Gaps
                                                                 0
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fun on: Thu Sep 2 11:16:54 1999; MasPar time 3.38 Seconds
56.561 Million cell updates/sec

Title: >US-08-599-226-3
Description: (1-9) from USOWS99226.pep
Perfect Score: 66
Sequence: 1 QRYNRAPYX 9

Scoring table: PAM 150 Gap 15

earched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq35

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part11 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 16.526; Variance 49.437; scale 0.334

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	Length	DB	Ħ	Description	Pred. No.
1	66	100.0	9	27	W27585	Anti-TNF-alpha antibo	1.22e+00
2	66	100.0	9	27	W27562	Anti-TNF-alpha antibo	1.22e+00
ω	66		107	27	W27568		1.22e+00
4	61	92.4	9	27	W27579	Anti-TNF-alpha antibo	4.64e+00
ហ	61	92.4	9	27	W27575	_	4.64e+00
o	61	92.4	9	27	W27571	Anti-TNF-alpha antibo	4.64e+00
7	58	87.9	9	27	W27584		1.02e+01
æ	56	84.8	9	27	W27572		1.71e+01
9	54	81.8	263	4	R22957	Human proteasome comp	2.87e+01
10	54		269	_	R22666	Protein used to raise	2.87e+01
11	51	77.3	9	27	W27570	Anti-TNF-alpha antibo	6.14e+01
12	51	77.3	9	27	W27576	Anti-TNF-alpha antibo	6.14e+01
13	51	77.3	9	27	W27577	Anti-TNF-alpha antibo	6.14e+01
14	51	77.3	9	27	W27574	Anti-TNF-alpha antibo	6.14e+01
15	51	77.3	170	œ	R42371	Prod. of ORF5 of plas	6.14e+01
16	50	75.8	287	11	R59920	Human Fc-alpha-R.	7.89e+01

444	42	433 800	36 37	2 W 4 Z	33 2	31	30	28	27	25	24	23	22	21	20	19	18	17
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5.5.5	, 50 50 5	66.7 66.7	5.5	η. ω	. α	ω.	œ œ				9.	9	Ξ.	Ξ.		Ϊ.	٠.	5
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100	455	W06702 R56281 W58586	612	ສະພ	757	445	0 0	418	R71133	113	~	757	38	674	57	758	R75006	403
ronal cronal con of O	tion ACC synth G-protein adr	tial medium c tin-deacetyla an histamine	e 708 Vl amin in sequence c	product	Protein with lipase a Lipase of Geotrichum	n matK protein.	Neutral protease enco Sequence of neutral p	yte ki	Cytopismic tyrosine k	rosine kinase dom	acid sequence	alpha anti	p25A GDP Dissoci	carnosus nitrat	i-TNF-alpha a	-TNF-alpha ant	omato S-adenosyl-	Fc-alpha-R.
.43e	.43e+0	3.43e+02 3.43e+02 3.43e+02	.43e+0	.70e+0	.70e+0	.70e+0	.70e+0	.70e+0	.70e+0	.70e+0	.12e+0	.12e+0	. 66e	.66e+0	.66e+0	.66e+0	.01e+0	· m

## ALIGNMENTS

88888888	CCCPPP	PR RR PI PI PI	S C C C C C C C C C C C C C C C C C C C	RESULT
The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1290 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple	High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer Claim 20; Page 72; 102pp; English. The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).	10-FEB-1997; U02219. :	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	UT 1 W27585 standard: poptide: 9 AA

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                                                                                                WPT: 97-415302/38.

High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer PS Claim 9: Page 64: 102pp; English.

CT The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).

CC factor alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).

CC less and has a Koff rate constant of 1x10 power -8 M or class and has a Koff rate constant of 1x10 power -3 s power -1 or class and has a Koff rate constant of 1x10 power -3 s power -1 or class and has a Koff rate constant of 1x10 power -3 s power -1 or class and has a Koff rate constant of 1x10 power -3 s power -1 or class and has a Koff rate constant of 1x10 power -3 s power -1 or class and has a Koff rate constant of 1x10 power -3 s power -1 or class and has a Koff rate constant of 1x10 power -7 M or less. The Ab, which constitution activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid csclutists or nephrotic csclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic csclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, calcoholic, viral or fulminant hepatitis, coagulation toxicity. The characteristic or inflammatory bone disorders, bone resorption disease, constant or purchasion, scar tissue formation, scar tissue formation, constant or subjective adherence of this inflammatory bone disorders, bone modifical call constant or subjective adherence of this inflammatory bone disorders of this is the subject of this is the s
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997;
10-FEB-1997;
25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-1998 (LIEST CHAIR)
Anti-TNF-alpha antibody light chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Hight chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
cardiac disorder; coaquilation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allen DJ, Hoogenboom HRJM, Mankovich JA, McGuiness BT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone resorption disease; coagulation disturbance; burn; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9729131-A1.
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                                                                            leukocyte adhesion molecule-1 (ELAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference
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Similarity 100.0%;
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oogenboom HRJM, Kaymakcalan Z, Labkovsky B,
A, McGuiness BT, Roberts AJ, Sakorafas P,
Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
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US-599226.
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                                            (HUVEC).
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Pred.
0; M
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No. 1.22e+00;
                                                                                on human umbilical vein
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                                                                                                                                                                                                                                                                                             FIT High affinity antibodies against human TNF alpha - useful to inhibit PT High affinity antibodies against human TNF alpha - useful to inhibit PT NF alpha activity, e.g. to treat autoimmune diseases and cancer S Claim 15; Page 75; 102pp; English.

CT The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain variable region. The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1292 assay with an IC50 of 1x10 power -7 M or less The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrevaia, periodonnal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cells (HTVFC)
                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T88403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salfeld JG, Schoenhaut D, WPI; 97-415302/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment; sepsis; disease; autoimmune disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-TNF-alpha antibody light chain variable region. Human; tumour necrosis factor-alpha; TNF-alpha; antibody; light chain; variable region; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W27568 standard;
W27568;
                                                                                                                                                                                                                                                                                endothelial
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Pred. No. 1.22e+00;
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RESULT ID W: AC W:

LT 4 W27579 standard; peptide; W27579;

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Best Local S
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High affinity antibodies against human TNF alpha - useful 1 High activity e.g. to treat autoimmune diseases and claim 20; page 70; 102pp; English.

The present sequence is a novel anti-human tumour necrosis. The present sequence is a novel anti-human tumour necrosis.
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Anti-TNF-alpha; antibody; CDR3;
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Hight chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
cardiac disorder; alease coagulation disturbance; burn; ELAM-1;
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The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
                                                                                                    Anti-TNF-alpha antibody light chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Hight chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
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09-FEB-1996; US-599226.
(BADI ) BASF AG.
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                                       keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
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10-FEB-1997; U02219
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Pred. No. 4.64e+00;
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Best Local
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14-AUG-1997
10-FEB-1997; U02219
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 69; 102pp; English.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.

High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 68; 102pp; English.
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

light chain; complementarity determining region 3; inhibition;

treatment; sepsis; disease; autoimmune disease; infectious disease;

treatment; sepsis; disease; autoimmune disease; infectious disease;

malignancy; pulmonary disorder; intestinal disorder; hepatitis;

cardiac disorder; inflammatory bone disorder; reperfusion injury;

bone resorption disease; coagulation disturbance; burn; ELAM-1;
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
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The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M
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Pred. No. 4.64e+00;
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RESULT ID WZ AC WZ
                                                                          R WPI 97-415302/38.

If WPI 97-415302/38.

If High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer SC Claim 20; page 72; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Koff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmon resonance), and CC less (both determined by surface plasmon resonance), and CC less (both determined by surface plasmon resonance), and CC constaltes human TNF-alpha cytotoxicity in a standard in vitro CC L929 assay with an ICSO of 1x10 power -7 M or less. The Ab, which CC inhibits TNF-alpha activity, rheumatoid arthritis, rheumatoid atthritis, rheumatoid atthritis, rheumatoid atthritis, rheumatoid here.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
light chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell loukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
                                              spondylitis, osteoarthritis, gouty arthritis, allergy, multiple scierosis, autoimmune diabetes, autoimmune uveitis or nephrotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W27584 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complem determining region 3 (CDR3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BADI )
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|:|||||
1 QRYNRAPY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Pred. No. 4.64e+00;
1; Mismatches (
                                     autoimmune uveitis or nephrotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementarity
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                                                  PT High affinity e.g. to treat autoimmune diseases and cancer PS Claim 20; Page 68; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).

CC determining region 3 (CDR3).

CC determining region 3 (CDR3).

CC less and has a Koff rate constant of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and curvalises human TNF-alpha cytotoxicity in a standard in vitro less (both determined by surface plasmon resonance), and curvalises human TNF-alpha cytotoxicity in a standard in vitro less and has a Koff rate constant of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha cytotoxicity in a standard in vitro autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, cardiac or inflammatory bone disorders, bone resorption disease, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The hab also inhibits TNF-alpha induced expression of endothelial celliculus of the province adherica modern and province adherication.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BADI ) BASE AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salfeld JG, Schoen WPI; 97-415302/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injur; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-TNF-alpha antibody light chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
light chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
                  leukocyte adhesion endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W27572 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L9-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells (HUVEC).
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                  (HUVEC).
                                       molecule-1 (ELAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.9%;
75.0%;
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Pred. No. 1.02e+01;
2; Mismatches 0
                                     on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation disturbances, ion, scar tissue formation,
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                                       umbilical
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Query Match Best Local Similarity

Conservative

84.8%;

Score 56; DB 27; Pred. No. 1.71e+01; 1; Mismatches 1

Length 9;

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δ B

QRYNRAPY

qkyqrapy

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IRESULT
AC R3
DT 15
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KW H4
COS H4
OS H4
PP 25
PP 21
PP 25
PP 45
PP
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Best Local Similarity
6; Conserv
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                           Query Match
Best Local :
   Matches
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20-JUL-1990; JP-193313.
(SAKA ) OTSUKA PHARM KK.
WPI; 92-136767/17.
N-NSDB; Q23894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human proteasome - has specified aminoacid sequence and gene base sequence, used for e.g. investigation of Alzheimer's disease Claim 1; Page 1; 24pp; Japanese.
Human proteasome HC2 and its gene can be used in the investigation diagnosis, and treatment of diseases associated with proteasome abnormality such as cancers and Alzheimers disease.
Human proteasome is purified from the soluble liver fractions of human liver cell HepG2 cell. A probe was prepared, and a cDNA library constructed using plasmid Bluescript KS+. A clone was isolated and its DNA sequenced to give Q23894.
See also Q23894-7, R22957-60.
                                                                                                                                                            prosomal cell surface proteins
Claim 13; Fig 9; 34pp; English.
The 269 amino acid sequence is used to raise antibodies against the prosomal surface protein p33K. The anti-p33K antibodies raised against this protein can detect prosomal surface antigens. HIV infected cells express these proteins on their surface, thus the antibodies may be used to detect HIV infection and to determine whether T4 cells have been infected even before they are killed by HIV.

JT 9
R22957 standard; Protein;
R22957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1992.
10-OCT-1991; E01945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein used to raise anti-p33K antibodies. HIV; human immunodeficiency virus; promosom
                                                                                                                                                See
                                                                                                                                                                                                                                                                                                                                                                                                        Method for diagnosing HIV infection - comprises using immunochemical reagent contg. monoclonal antibodies as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q24128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROS-) PRO-SOMA SARL.
Bey F, Bureau JP, Scherrer
WPI; 92-167288/20.
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R22666 standard; Protein; 269 AA.
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   Local Similarity
nes 6; Conser
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                                                                                                                                             also
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HC5; HC8; HC9; Alzheimer's disease;
                                                                                                                                             even before R22665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%;
75.0%;
                           81.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 4; L
Pred. No. 2.87e+01;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus; promosomal;
Score 54; DB 1; L
Pred. No. 2.87e+01;
0; Mismatches 2
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                                                      Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell surface; p27K.
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                                                                                                                                                                                                                                                                                                                                                                                                        against
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Gaps
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RESULT
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(factor-alpha (TNR-alpha) antibody (Ab) light chain complementarity

(determining region 3 (CDR3).

(The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

(less and has a Koff rate constant of 1x10 power -3 s power -1 or

(less (both determined by surface plasmon resonance), and

(neutralises human TNF-alpha cytotoxicity in a standard in vitro

(less (both determined by surface plasmon resonance), and

(neutralises human TNF-alpha cytotoxicity in a standard in vitro

(less (both determined by surface plasmon resonance), and

(neutralises human TNF-alpha cytotoxicity in a standard in vitro

(less (both determined by surface plasmon resonance), which

(inhibits TNF-alpha activity, can be used to treat sepsis,

(autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

(spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

(surface), autoimmune diabetes, autoimmune uveitis or nephrotic

(syndrome, infectious diseases, malignancy, pulmonary, intestinal,

(cardiac or inflammatory bone disorders, bone resorption disease,

alcoholic, viral or fulminant hepatitis, coagulation disturbances,

burns, reperfusion injury, keloid formation, scar tissue formation,

(The transport of the tree of the tree of the transport of t
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Best Local :
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10-FEB-1997; U02219.

25-NOV-1996; US-031476.

09-FEB-1996; US-599226.

(BADI ) BASE AG.
W27576 standard; peptide; 9 AA.
W27576;
W27576;
W27576;
W27576 first entry)
Anti-TNF-alpha antibody light chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Human; tomour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
light chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-TNF alpha antibody light chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Hight chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 97-415302/38.
High affinity antibodies against human TNF alpha - useful
TNF alpha activity, e.g. to treat autoimmune diseases and
Claim 20; Page 67; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W27570 standard; peptide; W27570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
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|:|| |||
1 QRYNRAPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells (HUVEC).
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 27;
Pred. No. 6.14e+01;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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TRESULT ACCORDANCE WITH ACCORDANCE WAS ACCORDANCE WITH ACCORDANCE WAS ACCORDANCE 
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PI Salfeld JG. Schoenhaut D. Vaughan TJ, White M. Wilton AJ;
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
Claim 20; Page 69; 102pp; English.

CT he present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1292 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC ab also inhibits TNF-alpha induced expression of endothelial cell
CC cendothelial cells (HUVEC).

So Sequence 9 AA.
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Best Local
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25-NOV-1996; U
                                                                                                                                                                         19-MAR-1998 (first entry)

Anti-TNF-alpha antibody light chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

light chain; complementarity determining region 3; inhibition;

treatment; sepsis; disease; autoimmune disease; infectious disease;

malignancy; pulmonary disorder; intestinal disorder; hepatitis;

cardiac disorder; inflammatory bone disorder; reperfusion injury;

bone resorption disease; coagulation disturbance; burn; ELAM-1;

keloid formation; scar tissue formation; pyrexia; HUVEC;

periodontal disease; obesity; radiation toxicity;

endothelial cell leukocyte adhesion molecule-1;

human umbilical vein endothelial cell.
   10-FEB-1997;
25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
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                                                                                                                              Homo sapiens.
W09729131-A1.
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US-599226.
   US-031476.
US-599226.
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75.0%;
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factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
less (both determined by surface plasmon resonance), and
thibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, rhematoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diseases, malignancy pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation discurbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
lawkowth adhesion molocular (ELL) and the molocular (ELL)
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASE AG.
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Hight chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
factor-alpha (TNF-alpha) antibody (Ab) light chain complementari determining region 3 (CDR3).
The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M oless and has a Koff rate constant of 1x10 power -3 s power -1 or
                                                                                      Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.

HIGH affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 69; 102pp; English.

The present sequence is a novel anti-human tumour necrosis for present sequence is a novel anti-human tumour necrosis.
                                                                                                                                                                                                    Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                              keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
WO9729131-A1.
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
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75.08;
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D, Vaughan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 27;
Pred. No. 6.14e+01;
1; Mismatches 1
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                       a Kd of 1x10 power -8 M or
                                                                                             tumour necrosis
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                                                                      complementarity
                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to inhibit
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Solutions of the provided process of the protein street of the protein shown is see also R42370-86.

So Sequence 170 AA:
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                                                         Query Match
Best Local Similarity
Matches 6; Conser
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Best Local Similarity
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09-APR-1992; US-865050.

04-JUN-1992; US-893424.

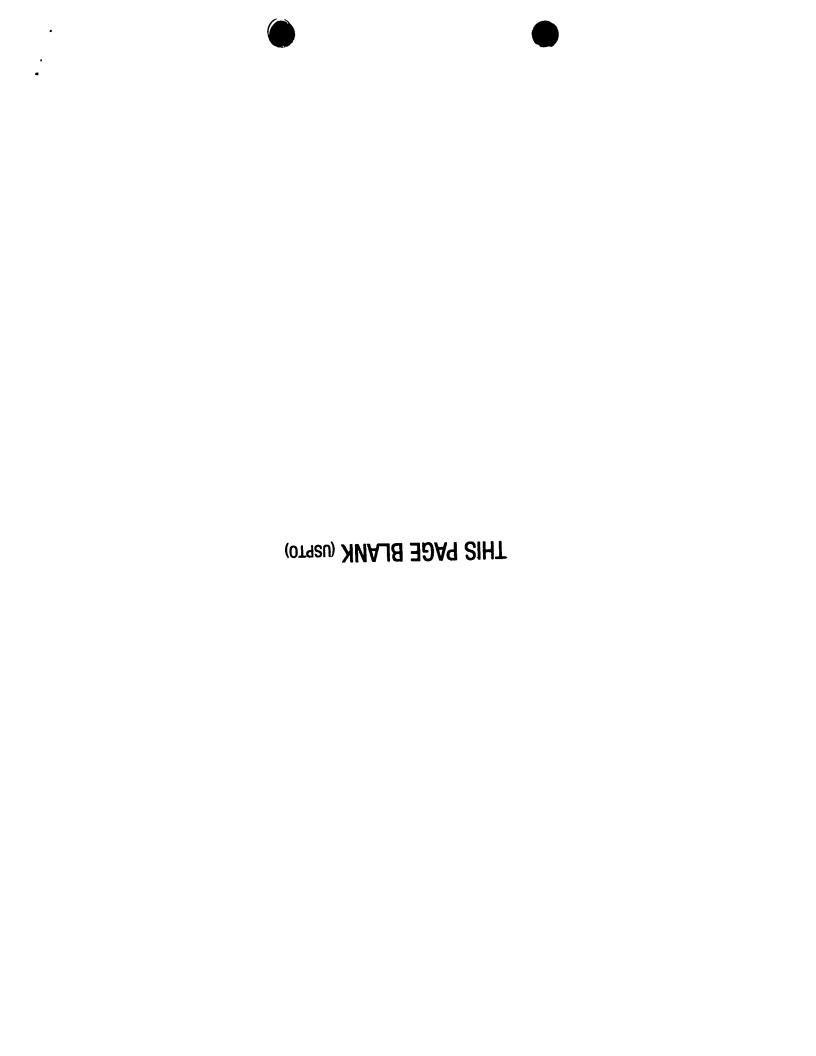
04-JUN-1992; US-893426.

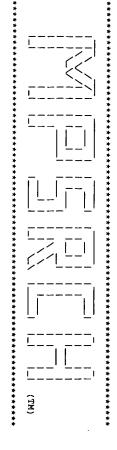
29-MAR-1993; US-038287.

29-MAR-1993; US-038719.
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R42371 standard; Protein; 170 AA.
R42371;
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Prod. of ORF5 of plasmid pRAP501.
Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; haemin-binging protein.
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N-PSDB; Q51080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rioux C, Theisen M;
WPI; 93-351733/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harland RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYSA-) UNIV SASKATCHEWAN.
Harland RJ, Pfeiffer CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus somnus.
107 qrykravy 114
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ilarity 75.0%;
Conservative
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ilarity 75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 27;
Pred. No. 6.14e+01;
1; Mismatches 1
                                                             Score 51; DB 8; L
Pred. No. 6.14e+01;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potter AA;
                                                                                                  Length 170;
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Ş 1 QRYNRAPY

Search completed: Thu Sep Job time : 18 secs. 2 11:17:12 1999





Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:20:18 1999; MasPar time 3.47 Seconds 73.528 Million cell updates/secondar output not generated.

Title: >US-08-599-226-4

Description: (1-12) from ueous999226.pep
Perfect Score: 66
Sequence: 1 VSYLSTASSLDX 12

Scoring table: PAM 150 Gap 15

earched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part26 37:part37 38:part38
39:part39

Statistics: Mean 16.837; Variance 49.496; scale 0.340

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIE

No.	Score 66	0 - Ch	Length	DB 27	ID W27594	Description Anti-TNF-alpha antibo	Pred. No
2	66	100.0	12	27	W27563		1.22e+00
ω	66	100.0	121	27	W27569		1.22e+0
4	58	87.9	12	27	W27593	-alpha	1.04e+0
ഗ	57	86.4	12	27	W27586	-alpha	1.35e+0
6	57	86.4	12	27	W27587		1.35e+01
7	57	86.4	12	27	W27589		1.35e+01
œ	57	86.4	12	27	W27588	-alpha	1.35e+0
9	52	78.8	441	32	W28236	Amino acid sequence o	4.92e+01
10	51	77.3	12	27	W27592	Anti-TNF-alpha antibo	6.34e+01
11	51	77.3	12	27	W27591		6.34e+01
12	49	74.2	12	27	W27590	Anti-TNF-alpha antibo	1.05e+0
13	48	72.7	417	26	W23067	Canine IgE heavy chai	1.35e+0
14	48	72.7	481	30	W40054	P300/CBP-associated t	1.35e+0
15	48	72.7	832	30	W40052		1.35e+0
16	48	72.7	,,,,			Human P300/CBP-associ	1 350+01

47 71.2 912 R61854 MBP peptide 14, poten 47 71.2 110 12 R61957 MBP peptide 14, poten 47 71.2 111 2 R61957 MBP peptide 14, poten 47 71.2 113 16 R85136 Human MBP residues 13 47 71.2 19 19 MBP 95335 MBP 1.1 (11-29). 47 71.2 19 373551 Human myelin basic pr 47 71.2 20 39 W73609 Human myelin basic pr 47 71.2 21 35 W78823 MBP-1.2 (11-31). 47 71.2 21 35 W78823 MBP-1.2 (11-31). 47 71.2 12 12 12 9 R48596 Rat myelin basic protein 47 71.2 1142 35 W38731 Streptococcus pneumon 47 71.2 1168 9 R48595 Myelin basic protein 47 71.2 166 9 R48595 Myelin basic protein 47 71.2 168 9 R48595 Myelin basic protein 57 12 170 9 R48595 Myelin basic protein 6 R30736 Human MBP. 47 71.2 170 9 R48595 Myelin basic protein 71.2 170 9 R48592 Human MBP. 47 71.2 170 19 R95406 Myelin basic pr 47 71.2 170 19 R95500 Human myelin basic pr 47 71.2 171 18 R99580 Human myelin basic pr 47 71.2 171 18 R99580 Human myelin basic pr 47 71.2 203 19 W06108 Foetal myelin basic pr 47 71.2 203 19 W06107 Foetal myelin basic pr 47 71.2 373 19 W06107 MP4 chimera (MBP21.5-47 71.2 385 19 W06107 MP4 chimera (MBP21.5-47 71.2 492 19 W06105 MM3GP4 chimera (MBP21.5-47 71.2 492 19 W06105	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
9 12 R61854 MBP peptide 2 10 12 R61957 MBP peptide 2 11 16 R85136 Human MBP rep 1	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47
12 R61854 MBP peptide 12 R61148 MBP peptide 12 R61157 MBP peptide 11 R615136 MBP peptide 11 R615136 MBP peptide 11 (11-30 11 (				•	•	•	•	•	٠	•	•	•	•			•	•	•	•	•	•	•	•	•	•	•	٠	•	•
2 R61854 MBP peptide: 2 R61948 MBP peptide: 2 R61957 MBP peptide: 2 R61957 MBP peptide: 2 R61957 MBP peptide: 6 R85136 MBP-1: (11: 6 R85136 MBP-1: (11: 7 W37551 Human myelin 9 W37550 Human myelin 9 W37550 Human myelin 5 W38731 MBP-1: 2 (11: 9 R48596 Rat myelin basic 9 R48596 Rat myelin basic 9 R48597 Myelin basic 9 R48598 MBP-1: 2 (11: 9 R48599 Human myelin 1 R04717 Empirically contained basic representation of the contained basic representation																												0	
MBP peptide  MBP peptide  MBP peptide  MBP peptide  MBP-11 (11:  MBP-11 (11:  MBP-1 (11:30  MBP-1.2 (11:30  MP4-1:10	19	5;	9	19	19	19	19	8	8	9	7	19	σ	<b>بس</b> ا	ø	ø	5	9	19	35	27	9	39	27	19	6	2	2	2
otide otide otide otide otide otide (11-30 (21-30 (31-30 (	$\sigma$	W06102	5	W06103	W06107	W06108	39	ın		R48592	R35440	R95406	R30736	R04717	R48594	R48595	W38731	R48596	R95336	W78823	W37550	(D	(4)		(n	(n	_	$\mathbf{L}$	6185
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# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.

WPI; 97-415302/38.

WPI; 97-415302/38.

WPI; 97-415302/38.

CE factor-alpha activity, e.g. to treat autoimmune diseases and cancer PS Claim 9; Page 65; 102pp; English.

CC factor-alpha (TWF-alpha) antibody (Ab) heavy chain complementarity CC factor-alpha (TWF-alpha) antibody (Ab) heavy chain complementarity CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less (both determined by surface plasmon resonance), and cutralises human TNF-alpha cytotoxicity in a standard in vitro CC 1293 assay with an IC50 of 1x10 power -7 M or less. The Ab, which CC inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid considerous, infectious diseases, malignancy, pulmonary, intestinal, CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC alcoholic, viral or fulminant hepatitis, coagulation toxicity. The CD burns, reperfusion injury, kaloid formation, scar tissue formation discusses.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; periodontal deal leukocyte adhesion molecule-1;
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Human; tumour necrosis factor-alpha; TNF-alpha;
Heavy Chain; complementarity determining region
       endothelial
Sequence
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09-FEB-1996;
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10-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human umbilical vein endothelial cell.
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                                                      leukocyte adhesion molecule-1 (ELAM-1)
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Similarity 100.0%;
11: Concerning 100.0%;
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US-599226.
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No. 1.22e+00;
                                                      on human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; CDR3
3; inhibition;
                                                      umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to inhibit
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                                                                                                                                                                                              High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer Claim 16; Page 76; 102pp; English.

Claim 16; Page 76; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain variable region. The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Koff rate constant of 1x10 power -3 s nod neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which is alsay with an IC50 of 1x10 power -7 M or less. The Ab, which cautoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple syndrome, infectious diseases, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disease, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The laukerte adhesion molecules, formation, scar tissue formation, allowed expression of endothelial cell
                                                                                            Query Match
Best Local
                                                                         Matches
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                                                                                                                                                                 leukocyte adhesion molecule-1 (ELAM-1)
endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salfeld JG, Schoenhaut D, WPI; 97-415302/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-TNF-alpha antibody heavy chain variable region Human; tumour necrosis factor-alpha; TNF-alpha; antiheavy chain; variable region; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W27569 standard;
W27569;
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Similarity 100.0%;
11; Conservative
                                                                                        n 100.08;
Similarity 100.08;
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                                                                         11;
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                                    109
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Pred.
0; M
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Pred. No. 1.22e+00;
0; Mismatches 0
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                                                                                        No. 1.
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                                                                                        DB 27;
1.22e+00
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RESULT

W27593 standard; peptide; 12 W27593;

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Alien DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Alien DJ, Hoogenboom HRJM, KGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; White M, Wilton AJ; Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; PJ-415302/38.

RWPI: 97-415302/38.

RWPI: 97-415302/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uery Match
                     malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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                                                                                                                                                                                                    Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
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10-FEB-1997; U02219.

25-NOV-1996; US-031476.

09-FEB-1996; US-599226.
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WO9729131-A1.
                                                                                                                                                                                                                                                                                   Anti-TNF-alpha
                                                                                                                                                                                                                                                                                                           19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                              W27586 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BADI ) BASF AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-TNF-alpha antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 sylstassle 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SYLSTASSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.98;
90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58; DB 27;
Pred. No. 1.04e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
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RESULT
ID W:
AC W:
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The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or 1 less and has a Koff rate constant of 1x10 power -3 s power -1 or 1 less (both determined by surface plasmon resonance), and 1 less (both determined by surface plasmon resonance), and 1 less (both determined by surface plasmon resonance), and 1 less (both determined by surface plasmon resonance), and 1 less (both determined by surface plasmon resonance), and 1 less (both determined by surface plasmon resonance), and 1 less (both determined by surface , surface 1 less (both determined by surface 1 less (both determined by surface), surface 1 less (both determined by surface), surface 1 less (both determined by surface 1 less (both determined by surface), surface 1 less (both determined by surface 1 less (both determined by surface), surface 1 less (both determined by surface), surface 1 less (both determined by surface 1 less (both determined by surface), surface 1 less (both determined by surface), surface 1 less (both determined by surface 1 less (both determined by surface), surface 1 less (both determined by surface 1 less (both determined by surface), and surface 1 less (both determined by surface 1 less (both determined by surface 1 less (both determined by surface), and surface 1 less (both determined by surface 1 less (both determined by surface 1 less (both determined by surface), and surface 1 less (both determined by surfa
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Best Local Similarity
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Salfeld JG, Schoenhaut D, V
WPI; 97-415302/38.
High affinity antibodies ag
TNF alpha activity, e.g. tc
Claim 20; Page 73; 102pp; F
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14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-0314/6.
09-FEB-1996; US-599226.
                                                                                                                                                                                                       14-AUG-1997
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                              periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour necrosis factor-alpha; TNN-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coaquiation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .T 6
W27587 standard; peptide; 12 AA.
W27587;
                                                                                                  Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton
                                                                                                                                                                                                                                                                                                              Homo sapiens. WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukocyte adhesion molecule-1 (ELAM-1)
endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain compleme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF alpha activity, e.g. t
Claim 20; Page 72; 102pp;
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Allen DJ, Hooger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-TNF-alpha antibody heavy chain CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High affinity antibodies against human TNF alpha - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mankovich JA, McGuiness BT,
                                                                                                                                                                                 (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%;
                             against human TNF alpha - useful to treat autoimmune diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB 27;
Pred. No. 1.35e+01;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treat autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                   pyrexia; HUVEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases
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                                                     to inhibit
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CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Koff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro CC le99 assay with an ICSO of 1x10 power -7 M or less. The Ab, which CC inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid cC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC alcoholic, viral or fulminant hepatitis, coagulation disturbances, CC pyrexia, periodontal disease, obesity and radiation toxicity. The CC ab also inhibits TNF-alpha induced expression of endothelial cell Cc leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein CC condition of the condition of t
                                           Allen D, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
WPI; 97-415302/38

RPI; 97-415302/38

RPI; 97-415302/38

RPI; 97-415302/38

The present sequence is a novel anti-human tumour necrosis
Claim 20; Page 73; 102pp; English.

The present sequence is a novel anti-human tumour necrosis
factor alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
Cdetermining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
Less and has a Koff rate constant of 1x10 power -3 s power -1 or
less and has a Koff rate constant of 1x10 power -3 not
less tobth determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
constant activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, rheumatoid
spondylitis, osteoarthritis, saltergy, multiple
scolerosis, autoimmune disbetes, autoimmune uveitis or nephrotic
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Best Local S
Matches
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; bene resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens. W09729131-A1.
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                               autoimmune diabetes, autoimmune uveitis or nephrotic
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90.0%;
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Pred. No. 1.35e+01;
1; Mismatches 0;
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                                                                    The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
determining region 3 (CDR3).
The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
constant is a standard in vitro
constant in vitro
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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W09729131-A1.
14-AUG-1997.
10-FEB-1997. U02219.
10-FEB-1996; US-031476.
09-FEB-1996; US-031476.
(BADI ) BASF AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-TNF-alpha antibody heavy chain CDR3;
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BADI ) BASF AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Allen DJ, McGuiness BT, Roberts AJ, Sakorafas P,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                         leukocyte adhesion molecule-1 (ELAM-1)
endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High affinity antibodies against human TNF alpha - TNF alpha activity, e.g. to treat autoimmune diseas Claim 20; Page 73; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-415302/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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l cells
12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l cells (HUVEC).
12 AA;
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Pred. No. 1.35e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases
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Query Match Best Local Similarity

86.4%; 90.0%;

Score 57; DB 27; Pred. No. 1.35e+01

Length 12

Mismatches

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Conservative

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                                                                                                                                                                                                     19-MAR-1998 (III'S ENLY)
Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
cardiac disorder; coaquiation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        based on homology with another Staphylococcus aureus protein, is believed to be a mercuric reductase. The DNA sequence was isolated from a library of clones of S. aureus WCUU 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus infection
Claim 6; Pages 547-548; 989pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP.
Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas Pratt JM, Reichard RW, Rosenberg M, Ward JM;
                                                                                                                    bone resorption disease; coagulation disturbance; keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against {\bf S}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9730070-A1.
21-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcal gene; regulatory element; bacterial vaccine; Staphylococcal infection; food poisoning;
                                   Homo sapiens.
W09729131-A1
                                                                                             human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W27592 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T84151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-FEB-1997; U02318.
20-FEB-1996; US-011888.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus protein; ribozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W28236;
07-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxic shock syndrome; mercuric reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a mercuric reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 vdyltstsale 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.8%;
                                                                                             endothelial cell.
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Pred. No. 4.92e+01;
5; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                        HUVEC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                 14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASE AG.
High affinity antibodies against h
TNF alpha activity, e.g. to treat
Claim 20; Page 74; 102pp; English.
The present sequence is a novel an
factor-alpha (TNF-alpha) antibody
                                                                                                                                                                 (BADI ) BASF AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Ankovich JA, McGuiness BT, Roberts AJ, Sakoraťas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                       Salfeld JG, Schoer WPI; 97-415302/38.
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W27591 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining region 3 (CDR3).
The Ab dissociates from TNF-alpha with a Kd of lx10 power -8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a novel anti-human tumour refactor alpha (TNF-alpha) antibody (Ab) heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone resorption disease; coagulation disturbance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.3%;
70.0%;
                                                                                         against human TNF al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 27;
Pred. No. 6.34e+01;
3; Mismatches 0
                              anti-human tumour necrosis
                                                                                            TNF alpha - usi
      heavy
      chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scar tissue formation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUVEC;
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   complementarity
                                                                                                                     useful
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                                                                                                                                                                                   AJ;
                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELAM-1;
                                                                                            to inhibit cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to inhibit
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Matches
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10-FEB-1997;
25-NOV-1996;
09-FEB-1996;
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                                                                                                            factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an ICSO of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                         (BADI ) BASF AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
WPI: 97-415302/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; keloid nisease; obesity; radiation toxicity; periodontal disease; obesity; radiation toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis,
                         sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease,
                                                                                                                                                                                                                                                                                                                    High affinity antibodies against human TNF alpha - useful 1 TNF alpha activity, e.g. to treat autoimmune diseases and claim 20; Page 74; 102pp; English.
The present sequence is a novel anti-human tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; heavy chain; complementarity determining disease; infectious disease; treatment; sepsis; disease; autoimmune disease; infectious disease;
                                                                spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
W09729131-A1.
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W27590 standard;
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Anti-TNF-alpha antibody he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endothelial cell leukocyte adhesion molecule-1;
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US-599226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide; 12
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 27;
Pred. No. 6.34e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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                                                                                                                                                                                                                                                                                               complementarity
                                                                                                                                                                                                                                                                                                                                                                  cancer
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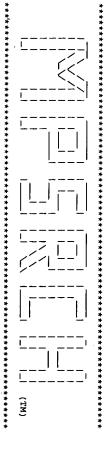
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                                                                                                    This polypeptide is encoded by exons 1-4 (see T79278) of IgE heavy chain constant region (epsilon) genomic DNA. A polypeptide, comprising the exon 5 and 6 product, is given W23068. Recombinant peptides encoded by exons 1-6 can be produced in eukaryotic or prokaryotic cells. Such pentide manifestation of the manifestation o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   burns, reperfusion injury, keloid formation, scar tissue formation pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-1998 (first entry)
Canine IgE heavy chain constant region (exon 1-4 product).
IgE; immunoglobulin; antibody; heavy chain constant region
allergy; hypersensitivity; therapy; dog; antisense;
immunomodulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
Misc_difference 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
Misc_difference 174
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Misc_difference 83
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Misc_difference 56
                                                                                                                                                                                                                                                                                                                                      WPI; 97-425031/39.
                                                                                                                                                                                                                                                                                                                                                           Harris RA,
                                                                                                                                                                                                                                                                                                                                                                         14-FEB-1997; U02322.
14-FEB-1996; US-601197.
(IDEX-) IDEXX LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc_difference
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Misc_difference 175
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                                                                         Sequence
                                                                                                                                                                                                                                                                                                   Isolated canine IgE heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9730156-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc_difference 55
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                                                                                           immediate
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Similarity 80.0%;
8; Conservative
                                                                         hypersensitivity,
417 AA;
                                                                                                                                                                                                                                                                                                                                                         Mermer B,
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? 67
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204
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203
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               72.78;
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Pred. No. 1.05e+02;
1; Mismatches 1
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                                                                                         dogs, e.g. to treatment for immunomodulation.
                 48; DB 26;
No. 1.35e+02;
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                                                                                                                                                                                                                                                                               region DNA -
allergies and
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                                Length 417
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Best Local Similarity
WO9803652-A2.
29-JAN-1998.
29-JUL-1997; U12877.
23-JUL-1996; US-022273.
(USSH) US DEDT HEALTH &
HOWARD BH, Nakattani Y;
WPI; 98-120777/11.
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P/CAF and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that inhibit or stimulate the transcription modulating and histone acetyltransferase activity of P/CAF and p300/CBB. Inhibitors can be used e.g. to inhibit HIV TAT-mediated transcription in the treatment of HIV infection. Stimulators can be used e.g. to activate tumour suppressor p53 in the treatment of cancer or to activate the muscle differentiation factor MyoD to promote muscle differentiation. The products can also be used to inhibit the cell cycle progression inducing effect of an oncoprotein which binds p300/CBB in a subject. The C-terminal fragment is specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated p300/CBP-associated factor, P/CAF - used to develop products for modulating transcription, e.g. for treating HIV infection or cancers or for promoting muscle differentiation Claim 2; Page 72-73; 107pp; English.

This polypeptide comprises the C-terminal region (amino acid residues 352-832) of a novel human p300/CBP associated cofactor, P/CAF (see W40052), that modulates transcription through binding to the cell transcription cofactors p300 (see W40055) and CBP (see W40050) and through acetylation of histones. This C-terminal region contains the histone acetyltransferase activity of the protein. The invention provides methods of screening for compounds that inhibit or efficients the histone acetyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human P300/CBP-associated transcriptional cofactor P/CAF. P/CAF; human; p300; CBP; transcription; cofactor; histone acetyltransferase; HIV; infection; cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W40052 standard; Protein; 832 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-1997; U12877.
23-JUL-1996; US-022273.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
HOWARD BH, NAKATANI Y;
                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muscle differentiation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W40052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1998 (first entry)
P300/CBP-associated transcriptional cofactor P/CAF C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W40054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /CAF; human; p300; CBP; transcription; cofactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 isynstsssle 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VSYLSTASSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBP in a subject. The C-terminal fragment is and can be used to identify and define P/CAF nce 481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           352..832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "contains binding site (Claim 2)"
                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.7%;
                                                                                            & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                      "contains histone acetyltransferase
activity (Claim 8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 30;
Pred. No. 1.35e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for p300/CBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Search completed: Thu Sep
Job time: 19 secs.
                                                                                                                                                                                                                                                                                       designated P/CAF, that modulates transcription through binding to the cell transcription cofactors p300 (see W40055) and CBP (see W40060) and through acetylation of histones. Its amino acid sequence was deduced from a clone (see V10090) obtained from a clone (see V10090) obtained from a clone (see W40055) and CBP (see W40056) of P/CAF, which contains the binding site for p300/CBP. C and the C-terminal region (see W40054), which contains the histone acetyltransferase activity are also claimed. The invention provides methods of screening for compounds that inhibit or stimulate the C transcription modulating and histone acetyltransferase activity of P/CAF and p300/CBP. Inhibitors can be used e.g. to inhibit HIV TAT-mediated transcription in the treatment of HIV infection. Stimulators can be used e.g. to activate them uscle differentiation factor MyoD to promote muscle differentiation. The products can also be used to inhibit the cell cycle progression inducing effect can also be used for detection, screening assays and production of
                                                                                                                                                                      Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated p300/CBP-associated factor, P/CAF - used to develop products for modulating transcription, e.g. for treating HIV infection or cancers or for promoting muscle differentiation Claim 1; Page 71-72; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This protein is a novel human p300/CBP associated cofactor
                                                                                                                                                                                                                                                                                 transgenic animals.
                                                                                                          394 isynstsssle 404
                                                                                                                                                         72.7%;
Local Similarity 63.6%;
nes 7; Conservativo
                                                                                      _
                                                                                      VSYLSTASSLD
                                                                                                                                                                                                                                                             832 AA;
                                                                                    11
                      2 11:20:37 1999
                                                                                                                                                                    Score 48; DB 30;
Pred. No. 1.35e+02;
3; Mismatches 1
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 12:30:26 1999; MasPar time 3.46 Seconds 73.740 Million cell updates/sec

Title: >US-08-599-226-29
Description: (1-12) from USO8599226.pep
Perfect Score: 75
Sequence: 1 ASYLSTSSSLDY 12

Scoring table: PAM 150
Gap 15
Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
[:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part18 29:part29 30:part30 31:part31 32:part32 33:part38 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39

Statistics: Mean 17.262; Variance 57.060; scale 0.303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	% Query Match	Length	DВ	Ü	Description	Pred. No.
1	75	100.0	12	27	W27588	Anti-TNF-alpha antibo	4.55e-01
N	72	96.0	12	27	W27593	-TNF-alpha ant	9.58e-01
ω	69	92.0	12	27	W27592	-alpha	2.00e+00
4	69		12	27	W27591	TNF-alpha	2.00e+00
<sub>5</sub>	69		121	27	W27569	_	2.00e+00
6	67	89.3	12	27	W27590	_	3.26e+00
7	63		12	27	W27586	Anti-TNF-alpha antibo	8.55e+00
8	63		12	27	W27589	_	8.55e+00
9	63	84.0	12	27	W27587	Anti-TNF-alpha antibo	8.55e+00
10	57	76.0	12	27	W27563	_	3.53e+01
11	57	76.0	12	27	W27594	-	3.53e+01
12	54		159	37	W80222	Human succinate-ubiqu	7.08e+01
13	54	72.0	159	29	W55260	H. pylori ORF 06cp306	7.08e+01
14	54		177	29	W55472	H. pylori ORF 06cp306	7.08e+01
15	54		526	29	W55688	H. pylori ORF 09cp107	7.08e+01
16	54		875	28	W34987	Bankia gouldi endoglu	7.08e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	١,
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18	39	27	27	27	32	27	24	32	27	24	27	27													23	26	32	3 2
	W81867	W36489	W36495	W36496	W54368	W36497	W10729	W54367	W36486	W10728	W36488	W36485	R58911	R87152	R87146	R58906	R08222	W71495	W06968	W17913	W24223	W17907	R39568	W01111	W19764	W23067	W59354	MORORO
s sarcoma	Human tumour suppress	Human TUB Form 1.	Form 2	Form 3	·O	Form 4	tub gene	e tub polype	щ	tub gene p	FC	H	Product of alternativ	Alternatively spliced	Protocadherin clone 4	Human protocadherin-4	Extracellular portion	Helicobacter polypept	M. tuberculosis ORF 2	Peptide CS4 from dena	Peptide fragment from		er.	HER-2/neu protein.		IgE heavy cha	n ErbB	7
.42e+0	.74e+0	. 74	.74e+0	.74e	.74e+0	.74e	.74e+0	.74e+0	.74e	÷	.74e+0	٠.	.20e+0	.20e+0	:٠	.20e+0	:.	:.	.20e+0	:.	.20e+0	:.	.76e+0	.76e+0	٠,	.76e+0		:

# ALIGNMENTS

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nniots TWF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple	neutralises human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which	less (both determined by surface plasmon resonance), and	factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CDR3)	2	High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer	WPI; 97-415302/38.	Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG. Schoenhaut D. Vaughan TJ. White M. Wilton AJ:	Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,	\9*EE=1990; US-299220. /*		14-AUG-1997.	HOMO Sapiens. WO9729131-A1.	human umbilical vein endothelial cell.	endothelial cell leukocyte adhesion molecule-1;	bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation: scar tissue formation: pureyia: HHVFC:	cardiac disorder; inflammatory bone disorder; reperfusion injury;	malignancy: pulmonary disorder: intestinal disorder: hepatitis:	heavy chain; complementarity determining region 3; inhibition;	Anti-TNF-alpha antibody heavy chain CDR3. Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;	19-MAR-1998 (first entry)	W27588 standard; peptide; 12 AA.	77 1

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PI Salfeld JG, Schoenhatt D, Vaughan TJ, White M, Wilton AJ;
PI High affinity antibodies against human TNF alpha - useful to inhibit
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
CC laim 20; Page 75; 102pp; English.

The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
CC less and has a Koff rate constant of 1x10 power -8 M or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1293 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, rheumatoid
CC sclerosis, autoimmune diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC succession, periodontal disease, obesity and radiation toxicity. The
CC andothelial colls (HUVEC) (ELAM-1) on human umbilical vein
CC endothelial colls (HUVEC)
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Matches 1
  Query Match
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25-NOV-1996; 1
09-FEB-1996; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BADI ) BASF AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disease; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W27593 standard; peptide; 12 AA W27593;
                                                                                    endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1998 (first entry)
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Similarity 100.0%;
12; Conservative
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US-031476.
US-599226.
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Score
Pred.
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Pred. No. 4.55e-01;
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  No.
  DB 27;
9.58e-01
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                                                                                                                                                                                                                                                                                                                                                 The present sequence is a novel anti-human tumour necrosis
factor-alpha (TWP-alpha) antibody (Ab) heavy chain complementarity
determining region 3 (CDR3).

The Ab dissociates from TWF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TWF-alpha cytotoxicity in a standard in vitro
neutralises human TWF-alpha cytotoxicity in a standard in vitro
1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
inhibits TWF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
Ab also inhibits TWF-alpha induced expression of endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                              Query Match
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.

High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BADI ) BASE AND (BADI ) HOOGENDOOM HRJM, Kaymako Allen DJ, HOOGENDOOM HRJM, Kaymako Mankovich JA, McGuiness BT, Robert Mankovich JA, McGuiness BT, Robert Mankovich JA, McGuiness BT, Robert Mankovich JA, Vaughan
                                                       W27591 standard; peptide; 12 AA. W27591;
                                                                                                                                                                                                                                                                                                 leukocyte adhesion molecule-1 (ELAM-1) endothelial cells (HUVEC).
Sequence 12 AA;
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25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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W09729131-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W27592 standard;
W27592;
                     Anti-TNF-alpha
                                          19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-1998
                                                                                                                                                                                                                                             Local
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                                                                                                                                                   1 ASYLSTSSSLDY
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                                                                                                                                                                                                                          Similarity 83.3% 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                        (first entry)
                     antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide; 12
                                                                                                                                                                                                                                           92.0%;
/ heavy chain CDR3.
factor-alpha; TNF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaymakcalan Z, Labkovsky
, Roberts AJ, Sakorafas P,
                                                                                                                                                                                                                      Score 69; DI
Pred. No. 2.0
2; Mismatcl
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                                                                                                                                                                                                                          Mismatches
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TNF-alpha; antibody; CDR3;
                                                                                                                                                                                                                                                            DB 27;
                                                                                                                                                                                                                                                                                                                                     on human umbilical
                                                                                                                                                                                                                                           .00e+00;
                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                          Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to inhibit cancer
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PPF 11
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High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer CC laim 20; Page 74; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Koff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro CC 1292 assay with an IC50 of 1x10 power -7 M or less. The Ab, which CC inhibits TNF-alpha activity, can be used to treat sepsis, CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC syndrome, infectious disease, autoimmune uveitis or nephrotic CC syndrome, infectious disease, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bune disorders, bone resorption disease, CC burns, reperfusion injury, keloid formation, scar tissue formation, CC about a periodontal disease, obesity and radiation toxicity. The CC andothelial cells (HUMPE)
                                                                                                                                                                         malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                    W27569;
19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone resorption disease; coagulation disturbance; burn; l
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitits; cardiac disorder; inflammatory bone disorder; reperfusion injury;
                                                                                                                                                                                                                                      Anti-TNF-alpha antibody heavy chain variable region.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
heavy chain; variable region; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                           W27569 standard; Protein; 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial cells (HUVEC).
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WO9729131-A1.
                                           Homo sapiens.
WO9729131-A1.
                                                                                                           endothelial cell leukocyte adhesion molecule-1;
                                                                                                                               keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
                                                                                    human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; DB 27;
No. 2.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 12;
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CCCCCSTTRICTORY
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The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain variable region. The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1292 assay with an IC50 of 1x10 power -7 M or less. The Ab, which is TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diseases, maignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The heal also inhibits TNF-alpha induced expression of endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
Claim 20; Page /4; IVAFF, The present sequence is a novel anti-hu factor-alpha (TNF-alpha) antibody (Ab)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BADI ) BASE AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z,
Mankovich JA, McGuiness BT, Roberts AJ, Si
Salfeld JG, Schoenhaut D, Vaughan TJ, Whi
WPI: 97-415302/38.
                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
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                                                                     High affinity antibodies against human TNF alpha activity, e.g. to treat auto-
Claim 20; Page 74; 102pp; English.
                                                                                                                                 Salfeld JG, Schoenhaut D, WPI; 97-415302/38.
                                                                                                                                                                                                                               14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                            Homo sapiens.
W09729131-A1.
                                                                                                                                                                                                                                                                                                                                                 keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W27590 standard;
W27590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukocyte adhesion molecule-1 (ELAM-1) on human umbilical endothelial cells (HUVEC).
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                                                                                                                                                                                                               BASF AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 cells
121 AA;
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US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%;
                                                                       to treat autoimmune English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69; DB 27;
Pred. No. 2.00e+00;
1; Mismatches 0
                                                    anti-human tumour necrosis
                                    heavy
                                                                                                             TNF alpha
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                                                                                             diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 121;
                                                                                                               useful
                                  complementarity
                                                                                           and
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                                                                                             cancer
                                                                                                             to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                     High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer SC claim 20; Page 72; 102pp; English.

CT The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CDR3).

CT The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Koff rate constant of 1x10 power -7 and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1292 assay with an IC50 of 1x10 power -7 M or less. The Ab, which cinhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 1
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W27586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld UG, Schoenhaut D, Vaughan TJ, White M, Wilton WPI: 97-415302/38
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone recorption disease; coagulation disturbance; burn; ELAM-1;
                        sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances,
                                                                                                          autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 27;
Pred. No. 3.26e+00;
0; Mismatches 1
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                                                                                    CT The present sequence is a novel anti-human tumour necrosis CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Koff rate constant of 1x10 power -3 s power -1 or CC neutralises human TNF-alpha cytotoxicity in a standard in vitro CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which CC inhibits TNF-alpha activity, can be used to treat sepsis, CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid compondylitis, osteoarthritis, gouty arthritis, rheumatoid conjuities, autoimmune diabetes, autoimmune uveitis or nephrotic CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC alcoholic, viral or fulminant hepatitis, coagulation disturbances, CC pyrexia, periodontal disease, obesity and radiation toxicity. The CC burns, reperfusion injury, keloid formation, scar tissue formation, CC pyrexia, periodontal disease, obesity and radiation toxicity. The CC ab also inhibits TNF-alpha induced expression of endothelial cell CC endothelial cells (HUVEC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilt WPI; 97-415302/38.

High affinity antibodies against human TNF alpha TNF alpha activity, e.g. to treat autoimmune diseas Claim 20; Page 73; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell
                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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l Similarity 100.0
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Similarity 100.0%;
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JA, McGuiness BT, Roberts AJ, Sakorafas P,
G, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
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No. 8.55e+00;
              DB 27;
8.55e+00;
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RESULT
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The Ab dissociates from TNF-alpha with a Kd of Ix10 power -8 M or less and has a Koff rate constant of Ix10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of Ix10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, burns, reperfusion injury, keloid formation, coagulation disturbances, burns, reperfusion injury, keloid formation, car tissue formation, over the content of the content of the coagulation disturbances.
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
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         Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; cardiac disorder; inflammatory bone disorder; reperfusion injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.

High affinity antibodies against human TNF alpha - useful t TNF alpha activity, e.g. to treat autoimmune diseases and c Claim 20; Page 73; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) autibody (Ab) heavy chain complements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  л 9
W27587 standard; peptide;
                                                                                                                                                                                            W27563 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                   19-MAR-1998 (first entry)
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Local Similarity 100.0%;
les 11; Conservative
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resorption disease;
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Pred. No. 8.55e+00;
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Best Local :
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
Allen DJ, Hoogenboom HRJ
 14-AUG-1997.
10-FEB-1997;
25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                               Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukcyte adhesion molecule-1 (ELAM-1) on human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal cardiac or inflammatory bone disorders, bone resorption disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an ICSO of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
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High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 9; Page 65; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factor alpha (TNF-alpha) antibody (Ab) heavy chain complem
                                                                                                                                                                                                                                                                                                                W27594 standard; peptide; W27594; 19-MAR-1998 (first entry)
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                                                                        Homo sapiens. 
W09729131-A1.
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                                                                                                                              endothelial cell leukocyte adhesion molecule-1;
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                                                                                                             human umbilical vein
                                                                                                                                         keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity;
                                                                                                                                                                                    bone resorption disease; coagulation disturbance;
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; U02219.
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; US-599226.
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                                                                                                             endothelial cell.
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Pred. No. 3.53e+01;
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                                                                                                                                                                pyrexia;
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R WPI; 97-415302/38.

Thigh affinity antibodies against human TNF alpha - useful to inhibity the second of the present sequence is a novel anti-human tumour necrosist factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CDR3).

C The present sequence is a novel anti-human tumour necrosist factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CDR3).

C The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and courtailses human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an ICSO of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimpuse diseases of the constant of the constant sepsis.
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Best Local
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20-MAR-1997; US-828832.
(INCY-) INCYTE PHARM INC.
Lal P, Shah P;
WPI; 98-593998/50.
N-PSDB; V66406.
                                                                                                             DNA encoding succinate-ubiquinone reductase membrane anchor subunit - useful for producing recombinant polypeptide Claim 1; Fig IA-B; 25pp; English.

The present sequence represents a human succinate-ubiquinone reductase membrane anchor subunit (SDHMA). The SDHMA nucleic acid sequence was first identified in Incyte clone 2454416 from the aortic endothelial cell cDNA library. The protein has chemical and structural homology with membrane anchoring subunits from bovine mitochondria, QPS3 and QPS1. The protein also contains potential intramolecular disulphide bridging sites, which are found at Cys11, Cys44, Cys88 and Cys150. SDHMA can be used to treat myopathies, e.g. progressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obbesity and radiation toxicity. The halso inhibits TNF-alpha induced expression of endothelial cell leukoyyte adhesion molecule-1 (ELAM-1) on human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; succinate-ubiquinone reductase membrane anchor subunit; SDHWA; Human; succinate-ubiquinone reductase membrane anchor subunit; SDHWA; myopathy; progressive external phthalmoplegia; Kearns-Sayre syndrome; myoclonic epilepsy; ecephalopathy; cardiomyopathy; lactic acidosis.
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Allen DJ,
                                                           external phthalmoplegia, Kearns-Sayre ecephalopathy, cardiomyopathy or lacti Sequence 159 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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A, McGuiness BT, Roberts AJ, Sakorafas
Schoenhaut D, Vaughan TJ, White M, Wil
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Pred. No.
Score
Pred.
                                                                            sayre syndrome, myoclonic lactic acidosis
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54;
No.
DB 37;
7.08e+01;
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3.53e+01;
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                                                                                                                                                                                                                                                                                                                                                                              PT helicobacter pylori nucleic acid sequences and encoded princection and for diagnosis of H. pylori infection PS Claim 14; Page 502; 1145pp; English.

CC This sequence is a H. pylori protein of unspecified function. PS Claim 14; Page 502; 1145pp; English.

CC The protein may be used in a vaccine to prevent or treat H. pylori PS Claim 14; Page 502; 1145pp; English.

CC Unfection or to identify H. pylori polypeptide binding compounds, in the protein may be used in a vaccine to prevent or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC Unit of the protein of the pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and CC can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions confided for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR compliant for recombinant polymentide production.
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06-DEC-1996; US-761318.

29-MAR 1996; US-625811.

02-APR-1996; US-758731.

25-OCT-1996; US-738905.

28-OCT-1996; US-738859.
                 24-JUN-1998 (first entry)
24-JUN-1998 (first entry)
H. pylori ORF 06cp30603_23452_c3_80 inner membrane protein.
Cytoplasmic; vaccine; prevention; treatment; infection; entricitation; binding compound; bacteria; life cycle; action: dindenal ulcer disease; chronic gastritis; diag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W55260;
Helicobacter pylori. W09737044-A1.
                                                                                                                 W55472 standard;
W55472;
                                                                                                                                                                                                                                                                                                                                                       amplification for recombinant polypeptide production, e.g. in hosts.
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Alm RA, Smith D;
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No. 7.08e+01;
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PT Helicobacter pylori nucleic acid sequences and encoded PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection PT infection and for diagnosis of H. pylori infection PT infection and for diagnosis of H. pylori infection PS Claims 14,80; Page 679; 1145pp; English.

CC This sequence is a H. pylori cell envelope inner membrane protein CC involved in cofactor metabolism.

CC The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and complementary to the DNA act as antisense sequences and the used to prevent the translation of H. pylori mRNA. Antibodies and distribution of H. pylori-specific antigens. The genomic sequence of the pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for significant homology to other known or exported computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted coding regions of interest, particular regions can be isolated from H. pylori by PCR complements. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR complements.
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09-OCT -1997. U05223.
27-MAR-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-738953.
25-OCT -1996; US-738959.
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Alm RA, Smith D;
WPI: 97-503122/46.
N-PSDB; V24881.
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27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-OCT-1996; US-738059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-1998 (first entry)
07-JUL-1998 (first entry)
H. pylori ORF 09cp10713_23452_c3_195 inner membrane protein.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
identification; binding compound; bacteria; life cycle; activator;
identification; binding compound; bacteria; life cycle; activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JT 15
W55688 standard; Protein; 526 AA.
W55688;
Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent infection and for diagnosis of H. pylori infection Claims 14,80; Pages 947-948; 1145pp; English.

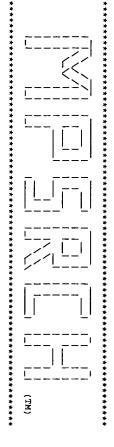
This sequence is a H. pylori cell envelope inner membran
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WPI; 97-503122/46.
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nes 6; Conservative
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Pred. No. 7.
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CC The protein may be used in a vaccine to prevent or treat H. pylori compounds, in the protein or to identify H. pylori polypeptide binding compounds, compounds of the protein or to identify H. pylori polypeptide binding compounds, compounds of useful as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC DNA and probes derived from it may be used for the identification of CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic cacid sequences complementary to the DNA act as antisense sequences and CC can be used to prevent the translation of H. pylori mRNA. Antibodies CC against the protein can be used in immunoassays to evaluate the abundance and istribution of H. pylori-specific antigens. The genomic sequence of CC H. pylori (ATCC 55679) was determined from overlapping contigs generated CC pylori (ATCC 55679) was determined from overlapping contigs generated CC mechanically shearing the bacterial DNA. The sequences were analysed for act least 180 nucleotides, and the predicted coding regions CC defined by computer evaluation. To identify likely H. pylori antigens for Vaccine development, the amino acid sequences predicted from various ORF combrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR camplification for recombinant polypeptide production, e.g. in E. coli nearly contact the protect of the coling the production of the pro
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Pred. No. 7.08e+01;
3; Mismatches 1
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Search completed: Thu Sep 2 12:30:47 1999 Job time : 21 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:33:13 1999; MasPar time 1.39 Seconds 87.360 Million cell updates/sec

bular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-599-226-29\_\_\_\_\_ (1-12) from USUB599226.pep 75 1 ASYLSTSSSLDY 12

Scoring table: PAM 150 Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 16.112; Variance 54.206; scale 0.297

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

esult No.	Score	Query Match	Length	DB	ID	Description		Pred. No.
1	54		158	2	US-08-828-	Sequence 3	, Applicatio	3.02e+01
2	54	72.0	159	N	-08-82	Sequence 1	plica	2e+
w	50		426	w	PCT-US95-1	Sequence 2	, Applicatio	. 56
4	50		426	<b>ب</b>	œ	Sequence 2	lic	5
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11	50	σ.	1255	N	US-08-356-	Sequence 2	•	7.5
12	49	5	37	ω	PCT-US96-0	Sequence 5	, App	٠.
13	49	5	117	ω	PCT-US96-0	Sequence 1	o	
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16	49	5	1026	_	US-08-453-	G	5	٠,
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18	49		1026	ш	US-07-998-	Sequence 9	5, Applicati	٠.
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49 65.3 1203 1 US-08-453 Sequence 103, Applicat 49 65.3 1203 1 US-08-453 Sequence 103, Applicat 49 65.3 1203 1 US-08-453 Sequence 203, Applicatio 48 64.0 4459 2 US-08-630 Sequence 2, Applicatio 48 64.0 4460 2 US-08-631 Sequence 7, Applicatio 48 64.0 460 2 US-08-630 Sequence 7, Applicatio 48 64.0 505 2 US-08-630 Sequence 2, Applicatio 48 64.0 505 2 US-08-936 Sequence 4, Applicatio 48 64.0 505 2 US-08-936 Sequence 2, Applicatio 48 64.0 505 2 US-08-935 Sequence 2, Applicatio 48 64.0 505 2 US-08-929 Sequence 2, Applicatio 48 64.0 506 2 US-08-936 Sequence 8, Applicatio 48 64.0 506 2 US-08-937 Sequence 8, Applicatio 48 64.0 506 2 US-08-936 Sequence 27, Applicatio 506 2 US-08-936 Sequence 27, Applicatio 506 2 US-08-936 Sequence	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24
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US-08-453 Sequence 103 US-08-453 Sequence 103 US-07-998 Sequence 103 US-08-630 Sequence 2 US-08-714 Sequence 2 US-08-630 Sequence 7 US-08-630 Sequence 7 US-08-630 Sequence 2 US-08-936 Sequence 4 US-08-936 Sequence 4 US-08-936 Sequence 2 US-08-936 Sequence 2 US-08-936 Sequence 2 US-08-935 Sequence 2 US-08-936 Sequence 8 US-08-936 Sequence 8 US-08-937 Sequence 2 US-08-531 Sequence 2	290	561	506	506	506	506	506	505	505	505	505	505	505	505	460	460	459	459	1203	1203	1203
-08-453 Sequence 103 -08-453 Sequence 103 -08-630 Sequence 2 -08-714 Sequence 7 -08-630 Sequence 7 -08-630 Sequence 7 -08-630 Sequence 2 -08-630 Sequence 2 -08-630 Sequence 2 -08-631 Sequence 2 -08-829 Sequence 2 -08-829 Sequence 2 -08-829 Sequence 2 -08-831 Sequence 8 -08-936 Sequence 8 -08-936 Sequence 8 -08-9374 Sequence 8 -08-936 Sequence 8	ωĸ	0	ب	N	N	N	N	ш	Ν	N	N	N	Ŋ	N	N	N	N	N	_	_	<u>_</u>
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	27, App	27, App	8, Appl	8, App	8, App	8, Appl	80	'n	2	2	4	2,	4,	e 2,	e 7,	7,	'n	2, Ap	103,	103,	103, App
	1.49e+02 1.49e+02	1.19e+02	1.19e+02	1.19e+02	1.19e+02		1.19e+02	1.19e+02	٠	1.19e+02	<u>.</u>	1.19e+02	1.19e+02	1.19e+02	1.19e+02		1.19e+02	1.19e+02	9.48e+01		9.48e+01

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LENGTH: 158 amino acids TYPE: amino acid	CHARACTERISTICS:	INFORMATION FOR SEC ID NO: 3:	 TELEPHONE: 415-855-0555	TELECOMMUNICATION INFORMATION:	" NUMBER:	REGISTRATION NUMBER: 36,749		ATTORNEY/AGENT INFORMATION:	FILING DATE:	APPLICATION NUMBER:	_	FICATION	ith	APPLICATION NUMBER: US/08/828,832	LICATION DATA:	FastSEO	ß	¥	TYPE: Di	岩	3	ĸ	••	Palo Alto	174 Porter Drive	ADDRESSEE: Incyte Pharmaceuticals, Inc.		R OF SEQUENCES: 4	NVENTION		APPLICANT: Lal, Preeti		5 5827711	Sequence 3. Application US/08828832		Sequence 3 Application (IS/08828832)			XXXXXX	US-00-020-032-3 SIRNDARD; FRI; IJO AR.	1 1 150 1 150

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1,
Patent No. 5
GENERAL INF
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08828832
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DOS
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,832
FILING DATE: Herewith
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                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                             STRANDEDNESS: S
TOPOLOGY: linea:
IMMEDIATE SOURCE:
LIBRARY: Consen:
CLONE: 2454416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: Linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1575011
JENCE 158 AA; 17096 MW; 135076 CN;
                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lal, Preeti
APPLICANT: Shah, PUTV1
TITLE OF INVENTION: NOVEL SUCCINATE DEHYDROGENASE SUBUNIT
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                           STREET: 3174 PORT
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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                                                                                       LENGTH:
TYPE: a
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                                       159 AA; 17043 MW; 129477 CN;
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                                                                                       H: 159 amino acids
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     72.0%;
larity 50.0%;
Conservative
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larity 50.0%;
Conservative
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                                                                                                                               415-845-4166
                                                      Consensus
                                                                       linear
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     Score 54; DB 2; I
Pred. No. 3.02e+01;
4; Mismatches 2
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Pred. No. 3.02e+01;
4; Mismatches 2;
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     Sequence 2, Application US/08336583 Patent No. 5629415
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Query Match 66.7%;
Best Local Similarity 63.6%;
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NAME: CARRY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 1921
TELECOMMUNICATION INFORMATION:
TELECHONE: (908) 594-6734
TELECAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9513795
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                                                                                                        US-08-336-583-2
Sequence 2, Application US/08336583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9513795
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
                                                                                                                                                                                                           214 TSYLSPPSPLD 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein JENCE 426 AA; 47234 MW; 1032622 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/13795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAHWAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 E. LINCOLN AVENUE;
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Pred. No. 7.56e+01;
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GENERAL INFORMATION:

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 1921:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEPAX: (908) 594-6730
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                    XXXXXX
                                                                                                                                                                                                                                                                                                            US-08-414-417B-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                            Sequence 68, Application US/08414417B
                                                                                                                                                                                                  Patent No.
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cheever, Marti
APPLICANT: Disis, Mary L.
CITY: Seattle
STATE: Washington
COUNTRY: US
COUNTRY: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                             TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCOD
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
ENCE 426 AA; 47234 MW; 1032622 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           ASYLSTSSSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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                                                                                       ADDRESSEE:
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llarity 63.6%;
Conservative
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                                                                         6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                       Cheever, Martin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                   Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA ENCODING CANINE IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/336,583
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Pred. No. 7.56e+01;
3; Mismatches 1;
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                                                                          701 Fifth Avenue
                                                                                                                                                                                                                                                                                                           1255 AA.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 68, Application US/08467083 Patent No. 5726023
                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 TYLPTNASLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SYLSTSSSLDY 12
                                                                                                                                                                                                                                                                               APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,41:
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 623-693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                             STREET: 6300 CONTY: Seattle STATE: Washing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                         APPLICATION NUMBER: US/08 FILING DATE: 06-JUN-1995 CLASSIFICATION: 424
                        REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
                                  NAME: Sharkey, Richa
REGISTRATION NUMBER:
                                                                                                                                                                                                                     COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sharkey, Richard G. REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                   6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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45.5%;
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682-6031
NO: 68:
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Pred. No. 7.56e+01;
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MOLECULE TYPE:
SEQUENCE 1255 AA
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63 TYLPTNASLSF 73
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TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 68:
                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                Local Similarity
                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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les 5; Conser
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MEDIUM TYPE: Floppy disk
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LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
JENCE 1255 AA; 137955 MW; 8109851
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                              STREET: 6300 CCCITY: Seattle STATE: Washing!
                                                                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                    TYPE:
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FILING DATE: 01-APR-1996
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                       <u>ن</u>
                                                                LE TYPE: protein
1255 AA; 137909 MW; 8111405 CN;
                                                                                                                                                                                                                                                                                                                                        98104-7092
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)GY: linear
                     Conservative
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Pred. No. 7.
5; Mismatc
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APPLICANT: Cheever, Martin
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE
TITLE OF INVENTION: FOR DIA
TITLE OF INVENTION: HER-2/n
                                          Sequence 8, Application US/08484438
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Sequence 8, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
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                                                                                                                                                                                    66.7%;
Local Similarity 45.5%;
les 5; Conservation
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INFORMATION FOR SEQ ID NO:
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2 SYLSTSSSLDY 12
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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GY: linear
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)O Columbia Center,
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Pred. No. 7.56e+01;
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GENERAL INFORMATION:

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                                                                                       Sequence 68, Application US/08468545B
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
DEBI TOTATION DATA: TECONOMICAL ACCORDING TO THE POLICATION DAT
Sequence 68, Application US/08468545B Patent No. 5876712 GENERAL INFORMATION:
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FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  63 TYLPTNASLSF 73
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
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APPLICANT: Siegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: unl
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07
CLASSIFICATION:
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1255 AA; 137815 MW; 8105484 CN;
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Pred. No. 7.56e+01;
5; Mismatches 1
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Best Local Similarity 45.5%;
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                                                                                                                                                                                              Sequence 2, Application US/08356786 Patent No. 5877305
                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      63 TYLPTNASLSF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
                                                                                                                                                                                                                                                                                                                                               2 SYLSTSSSLDY 12
                                                       CORRESONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz,
ADDRESSEE: Funhange Place, 53 State Street
                                                                                             APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Blosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino aci
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ADDRESSEE: Seed and Berry LLP
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Disis, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cheever, Martin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 COCITY: Seattle STATE: Washing:
                    COUNTRY:
ZIP: 021
                                           CITY: Boston
STATE: Massa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
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1255 AA; 137955 MW; 8109851 CN;
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                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
                                USA
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMUNE REACTIVITY TO HER-2/neu PROTEIN
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
HER-2/neu ONCOGENE IS ASSOCIATED
69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/468,545B
                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 2;
Pred. No. 7.56e+01
5; Mismatches
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COMPUTER:

IBM

PC compatible

PatentIn Release #1.0, Version #1

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 1255 AA; 137909 N
                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application PC/TUS9608730
                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US96-08730-5
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                            Sequence 5, Application PC/TUS9608730 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TYLPTNASLSF 73
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/831,96

FILING DATE: 06-FEB-1992

ATTORNEY_AGENT INFORMATION:

NAME: Pitcher, Edmund R.

REFERENCE/DOCKET NUMBER: CRP-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SYLSTSSSLDY 12
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
         ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: PCT/US96/08730
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        APPLICANT: Cassels, Frederick
APPLICANT: Anderson, Jeffrey
APPLICANT: Carter, John Mark
TITLE OF INVENTION: Methods of Raising
TITLE OF INVENTION: Coli of the Family
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                          STATE: VA
COUNTRY: US
ZIP: 22031
                                                                   FILING DATE: 0
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                             Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                        E: Glenna Hendricks
P.O. Box 2509
                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.5%;
                                                                              03-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                           PCT/US96/08730
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Pred. No. 7.56e+01;
5; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 591-4428
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                       TELEFAX: (703) 591-4428
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                CLASSIFICATION:
ATTORIEY/AGENT INFORMATION:
ATTORIEY AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: PCT/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 591-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 GSYLPTAVELTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASYLSTSSSLDY
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TOPOLOGY: unknow
MOLECULE TYPE: pel
HYPOTHETICAL: NO
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glenna Hendricks
FRAGMENT TYPE: internal ENCE 117 AA; 12389 MW; 76297 CN;
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Carter, John Mark
TITLE OF INVENTION: Methods of Raising
TITLE OF INVENTION: Coli of the Family
                        HYPOTHETICAL: N
                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               COUNTRY:
ZIP: 220
                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 03-JUI
                                                                  TYPE: amino STRANDEDNESS:
                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                  STATE:
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Anderson, Jeffrey
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Pred. No. 9.48e+01
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Best Local S
Matches
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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                           MOLECULE TYPE: ORF2 protein SEQUENCE 384 AA; 41963 MW; 701271 CN;
           XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXXX
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                                 PCT-US95-08071-95
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                                                                                                    235 SSYLPTKAALD 245
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Local Similarity 50.0%;
hes 6; Conservative
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                                                                                                                                                                                                                                                  TELEFAX: (415) 543-504 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                               1 ASYLSTSSSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ASYLSTSSSLDY 12
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: LENGTH: 384 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA INVOLVED TITLE OF INVENTION: IN THE BIOSYNTHESIS OF CYCLOPROPANATED MYCOLIC ACIDS TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BARRY III, Clifton E. APPLICANT: YUAN, Ying
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 NAME: Chambers, Guy W. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Steuart Stre
                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                              amino acid
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                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Townsend and Townsend Khourie and Crew
Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                          384 amino acids
                                                                                                                                                                                                                                                (415) 543-5043
(415) 543-5043
                                                                                                                                                                                                  linear
                                                                                                                                         65.3%;
54.5%;
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                                 STANDARD;
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                                                                                                                            Score 49; DB 1; Len
Pred. No. 9.48e+01;
4; Mismatches 1;
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Pred. No. 9.48e+01.
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                                 1026 AA
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                                                                                                                                                  Length 384;
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Best Local (
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                                                                423 FLQTTTPLDY 432
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                                                                                                                                                                           TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino aci
                                                                                                 Local Similarity
                                          3 YLSTSSSLDY 12
                                                                                                                                MOLECULE TYPE
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 321
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/998,003 FILING DATE: 29 DEC 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         FILING DATE: 23 DEC 1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                        TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                    NAME: Noland, Greta E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/08071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60606
                                                                                                                                                                amino acid
                                                                                                                                             TYPE:
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                            1026 amino acids
                                                                                                                                 AA; 111270 )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                       linear
                                                                                                 65.3%;
          2 12:33:21 1999
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                                                                                                                                                                                                                                                                                                                                                PCT/US93/12588
                                                                                                                                  MW; 5611711 CN;
                                                                                                 Score 49; DB 3; I
Pred. No. 9.48e+01;
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                                                                                                                                                                                                                                                         32149
                                                                                      Mismatches
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                                                                                                           Length 1026;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:31:04 1999; MasPar time 3.15 Seconds 152.820 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Title: >US-08-599-226-29 (1-12) from USO8599226.pep 75 1 ASYLSTSSSLDY 12

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 24.557; Variance 30.670; scale 0.801

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

NO.	Score	Query	Length	DB	ID	Description	Pred. No.
₽,	54	72.0	503	ผ	F64713	protein-export membra	2.65e+00
2	54		526	N	D71805		•
ω	53	70.7	265	N	S38380	٠	
4	52		917	L	ACGAE	ate receptor p	
ر.	51		471	N	C71439	-	
σ	51		1069	N	T00040	ന	1.05e+01
7	51		1069	N	T00043	BH-protocadherin-a -	1.05e+01
8	51		1072	N	T00041	BH-protocadherin PCDH	1.05e+01
9	51		1200	N	T00042	BH-protocadherin PCDH	1.05e+01
10	50		293	N	D70108	conserved hypothetica	1.64e+01
11	50		469	N	D70048	ABC transporter (amin	1.64e+01
12	50		626	H	IKECB	colicin Ib - Escheric	1.64e+01
13	50	66.7	989	N	156333	apolipoprotein B - ra	1.64e+01
14	50		1186	N	T03180	tyrosine protein kina	1.64e+01
15	50		1255	L	A24571	protein-tyrosine kina	1.64e+01
16	49		105	N	S69755	hypothetical protein	2.54e+01
17	49		112	4	S59333		
18	49		377	N	F71520		2.54e+01
19	49		392	N	B70242	conserved hypothetica	2.54e+01
20	49		409	N	G64677	NADH dehydrogenase (u	2.54e+01
21	49		409	N	E71838	æ	2.54e+01
22	49		564	N	A38271	serotonin receptor 7	2.54e+01
23	49		650	2	F70974	probable acrAl protei	2.54e+01

.3 1469 2 A55095 .0 272 2 D64155 .0 297 2 G70708 .0 325 2 S75747 .0 428 2 A55004 .0 441 2 G70829 .0 475 2 S58519 .0 477 2 F71918 .0 505 2 S68518 .0 505 2 S68518 .0 1211 2 S54500 .1 211 2 S54500 .1 211 2 S54500 .7 176 2 F70231 .7 593 2 C49525 .7 684 2 G71446 .7 186 2 F70231 .7 593 2 S49525 .7 684 2 G70744 .7 826 2 B36203 .7 963 2 A57238 .7 966 2 PC4208	45	44	43	42	41	40	39	38	37	36	35	34	<u>3</u> 3	32	31	30	29	28	27	26	25	24
1469 2 Ab5095 chromosome condensa 272 2 D64155 hypothetical protein 297 2 G70708 probable purC proces 297 2 G70708 probable purC proces 297 2 G70708 probable secry protein 428 2 A55044 beta-4C-adrenergic 441 2 G70822 probable secry protein 441 2 G70822 probable secry protein 475 2 S58519 hypothetical protein 505 2 S68518 hypothetical protein 505 2 S68518 tub protein, brain 1792 2 S68518 tub protein dehydrogen 954 2 G71496 hypothetical protein 1211 2 S54500 alpha,alpha-trehala 1791 2 S65534 conserved hypothetical protein 1791 2 S65534 conserved hypothetical protein 62 C C25035 colicin Ia - Escher 505 2 C35035 colicin Ia - Escher 636 2 C35035 colicin Ia - Escher 636 2 C35035 iron-responsive ele 963 2 A57238 iron-responsive ele 976 2 PG4208 valinetrna ligase	47	47	47	47	47	47	47	47	47	48	48	48	48	48	48	48	48	48	48	48	48	49
2 A5595 2 Chromosome condensa 2 D64155 3 Pypothetical protein 2 G70708 2 probable purC proce 2 S75747 3 hypothetical protein 2 A5504 4 beta-4C-adrenergic 2 G7082 2 probable secv protein 2 S58519 3 hypothetical protein 3 F71918 4 hypothetical protein 5 F71918 5 hypothetical protein 2 F71918 5 hypothetical protein 3 F71918 6 hypothetical protein 5 G71496 6 hypothetical protein 6 G71496 7 Light-harvesting che 7 F70231 7 Conserved hypothetical 7 S49525 7 Colicin Ia - Eschery 2 G70744 7 hypothetical protein 2 G70744 7 hypothetical protein 3 T03030 8 iron-responsive ele 8 PC4208 8 valinetRNA ligase	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0			64.0	64.0	65.3
A5095  A5095  Chromosome condensa D64155  hypothetical protei G70708  probable purC prote G77747  hypothetical protei A55044  beta 4C-adrenergic G70822  probable secv protei F71918  hypothetical protei F71919  hypothetical protei F71919  hypothetical protei F71919  hypothetical protei F71919  hypothetical protei F710231  conserved hypothetical F70231  glycoprotein G - si C25035  colicin Ia - Escher G70744  hypothetical protei G70744  hypothetical protei F70739  hypothetical protei	976	963	949	826	684	626	593	386	179	1211	954	814	505	477	475	459	441	428	325	297	272	1469
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onodensa protei C protei C protei protei certifica protei trehala trehala trehala trehala trepotei protei ive ele le protei live ele	PC4208	A57238	T03030	в36203	G70744	C25035	S49525	F70231	S65534	S54500	G71496	139627	S68518	F71918	S55093	S68519	G70822	A55044	S75747	G70708	D64155	A55095
	valinetRNA ligase (	iron-responsive eleme	hypothetical protein	iron-responsive eleme		Ia -	glycoprotein G - simi	conserved hypothetica	light-harvesting chlo	alpha,alpha-trehalase	hypothetical protein	nicotine dehydrogenas				tub protein, testis -	probable secY protein	beta-4C-adrenergic re	hypothetical protein	probable purC protein	hypothetical protein	chromosome condensati

# ALIGNMENTS

RESULT 2 ENTRY	Db 38 YLSLASALEY     : : :    Qy 3 YLSTSSSLDY	Query Match Best Local Similarity Matches 6; Conse	GENETICS #Start_codon CLASSIFICATION SUMMARY	##molecule_type DN ##residues 1- ##cross-references	##status	#cross-refere	#journal			#authors	ACCESSIONS REFERENCE	ORGANISM DATE	RESULT 1 ENTRY TITLE
D71805 #type complete	YLSTASALEY 47     : : :    XLSTSSSLDY 12	72.0%; Score 54; DB 2; Length 503; ilarity 60.0%; Pred. No. 2.65e+00; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	GTG #superfamily protein export membrane protein secD #length 503  #molecular-weight 54247  #checksum 3320	_type DNA 1-503 ##label TOM ferences GB:AE000652; GB:AE000511; NID:g2314720; PID:g2314730; TIGR:HP1550		rutite ine complete genome sequence of the gastric pathogen Helicobacter pylori. cross-references MUID:97394467 F64713	C.M.; Venter, J.C. Nature (1997) 388:339-547	J.1 Wattarpl	J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;	Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,	F64713 A64520	<pre>#formal_name Helicobacter pylori 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 12-Feb-1999</pre>	F64713 #type complete protein-export membrane protein - Helicobacter pylori (strain 26695)

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164-220
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

#journal Nature (1999) 397:176-180
Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #gene
                                                                                                                                                                                                                                               ##cross-references EMBL:X75217; NID:g407414; PID:g407415
IFICATION #superfamily unassigned homeobox proteins; homeobox homology
DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                         ##residues
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##cross-references GB:AE001567; GI
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Local Similarity 60.0%;
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                                                      ASYLSTSSSLDY 12
                                                                                                                                          70.7%;
Similarity 75.0%;
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                                                                                                                                                                                                                                                                                                                                                                             Degnan, B.M.; Degnan, S.M.; Morse, D.E.
submitted to the EMBL Data Library, September 1993
Expression of Hrox, a gastropod mollusc Hox homeobox gene,
progressively restricted during morphogenesis from
trochophore to veliger larval forms.
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S38380
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17-Oct-1997
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12-Feb-1999
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protein - California red abalone
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#molecular-weight 29579
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#molecular-weight 56796 #checksum 5813
                                                                                                                                          Score 53; DB 2; I Pred. No. 4.22e+00;
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Pred. No. 2.65e+00;
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CLASSIFICATION #superfamily glutamate receptor; glutamate receptor homology
KEYWORDS glycoprotein; ion channel; neurotransmitter receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references EMBL:X60086
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Best Local Similarity 54.5%;
Matches 6; Conservative
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559-578
599-617
628-646
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251,261,272,418,
419,424,491,881
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#accession S18443
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##residues 1-362,'K',364-776,'S',778-845,'R',847-886,'S',888-917
##label HU2
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Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveren, M.; Stlekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel, K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Gielen, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.; Lecharny, A.; Auborg, S.; Gy, I.; Kreis, M.; Lao, N.; Kavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hutton, M.L.; Bhandal, N.S.; Harvey, R.J.; Usherwood, Darlison, M.G. submitted to the EMBL Data Library, June 1991 PCR-mediated cloning of a cDNA that encodes a function molluscan glutamate receptor subunit.
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FEBS Lett. (1991) 292:111-114
Cloning of a CNMA that encode:
receptor subunit.
                                                                                                                                                                                                                                                               columbia
03-Aug-1998
                                                                                                                                                                                                                                                                                                                              C71439 #type complete
hypothetical protein - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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#formal_name Lymnaea stagnalis #common_name great pond snail
31-Mar-1992 #sequence_revision 28-Oct-1994 #text_change
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#domain transmembrane #status predicted #label TMI\
#domain transmembrane #status predicted #label TM2\
#domain transmembrane #status predicted #label TM3\
#domain transmembrane #status predicted #label TM4\
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#product glutamate receptor #status predicted #label
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h 917 #molecular-weight 103106
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bred. No. 6.67e+00;
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James, R.; Montfort, A.; Pons, A.; Puigdomenech, P.; Douka,
A.; Voukelatou, E.; Milloni, D.; Hatzoppulos, P.;
Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.;
Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.;
Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny,
M.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klosterman, S.;
Schueller, C.; Chalwatzis, N.
#journal Nature (1998) 391:485-488
#title of Arabidopsis thaliana.
#cross-references MUID:98121113
#accession C71439
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##residues 1-10
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Local Similarity 60.0%;
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Similarity 63.6%;
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#length 471 #molecular-weight 52785
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BH-protocadherin-a - mouse
#formal_name Mus musculus #common_name house mouse
22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change
22-Jan-1999
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Cloning, expression analysis,
BH-protocadherin (PCDH7), a
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BH-protocadherin PCDH7 - human
#formal_name Homo sapiens #common_name man
22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change
Yoshida,
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Pred. No. 1.05e+01;
3; Mismatches 1
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Pred. No. 1.05e+01;
3; Mismatches 1
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##molecule_type mRNA
##residues 1-1069 ##label YOS
               ##residues 1-1200 ##label YOS ##cross-references EMBL:AB006757; |
                                              ##molecule_type mRNA
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##residues 1-1072 ##label YOS
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##experimental_source clone BH-Pcdh-c
                                                                 ##status
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Local Similarity 60.0%;
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#length 1069
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Cloning, expression analysis, and chromosomal localization
BH-protocadherin (PCDH7), a novel member of the cadherin
                                                                                                                                                                                                                             T00042 #type complete
BH-protocadherin PCDH7 (clone BH-Pcdh-c) -
#formal_name Homo sapiens #common_name man
22-Jan-1999 #sequence_revision 22-Jan-1999
22-Jan-1999
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Cloning, expression analysis,
BH-protocadherin (PCDH7), a
superfamily.
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BH-protocadherin PCDH7 (clone BH-Pcdh-b) - human
#formal_name Homo sapiens #common_name man
22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change
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Pred. No. 1.05e+01
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##residues 1-293 ##label KLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artlach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C. Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                              Kunst, F.;
                                                                                                                                                                                                                                                                 #formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Borrelia burgdorferi #common_name Lyme disease
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unst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessleres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterboeft, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
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                                                                                                                                                                                                                                                                                                                             transporter (amino acid permease) homolog yvsH - Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary; nucleic acid sequence not shown
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Pred. No. 1.64e+01
4; Mismatches
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Pred. No. 1.05e+01
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Best Local Similarity 36.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal #title
                                                                                                                                                                                                                                                                                                                                                                            #cross-references MUID:85014128
#accession A93533
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#accession D700
     #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors
                                                                                                                           ##residues 1-626 ##label VAR ##cross-references GB:X01009; NID:g41141; PID:g41142 ##cross-references uthors translated the codon GAA ##note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Varley, J.M.; Boulnois, G.J.
Nucleic Acids Res. (1984) 12:6727-6739
Analysis of a cloned colicin IB gene: complete
sequence and implications for regulation of e
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#length 469 #molecular-weight 50258 #
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colicin Ib - Escherichia coli plasmid Colib
#formal_name Escherichia coli
17-Mar-1987 #sequence_revision 17-Mar-1987
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Mankovich,
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J.A.; Hsu, C.H.; Konisky, J.
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#title
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#journal Nucleic Acids Res. (1984) 12:8748
#contents annotation; corrigendum
#MMENT This bactericidal protein functions by depolarizing the
                                                                                                                                                                                                                                #accession
                                                                                                                                                                                                                                            #cross-references MUID:89176719
                                                                                                                                                                                                                                                                                                                 #authors
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#journal J. Biol. Chem. (1984) 259:8764-8768
#tille Organization of the colicin Ib gene
#cross-references_MUID:84264487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal J. Bacteriol. (1986) 168:228-236
#title DNA and amino acid sequence analysis of structural and immunity genes of colicins Ia and Ib.
#cross-references MUID:87008385
#accession D25035
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                                                                                                                                                                                          ##molecule_type mRNA
##resian--
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##residues 2-21 ##label MA3
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  YLSTSSSLDY 12
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Similarity 63.6%;
7; Conservative
                                                                     Similarity
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                                                                                                             apoB
#superfamily apolipoprotein
#length 989 #checksum 1918
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#superfamily colicin IB
antibiotic; bacteriocin;
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Biosynthetic relationships between
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                                                                                                                                                                                                                                                                                                           Reuben, M.A.; Svenson, K.L.; Doolittle,
                                                                                                                                                                                                                                                                                                                                                                     156333 #type fragment
apollpoprotein B - rat (fragment)
#formal_name Rattus norvegicus #cc
26-Jul-1996 #sequence_revision 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #product colicin Ib #status experimental #label
#length 626 #molecular-weight 69923 #checksum 8113
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                                                        Conservative
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ces GB:M27440;
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                                                                     66.7%;
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Pred. No.
2; Misma
                                                      Score 50; DB 2; L
Pred. No. 1.64e+01;
2; Mismatches 2
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NID:g623548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.64e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxin; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ib gene.
                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                        #common_name
26-Jul-1996 #
                                                                                                                                                                     PID:g623549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 626
                                                        2;
                                                                                    Length 989;
                                                                                                                                                                                                                GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                       three
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Konisky,
                                                                                                                                                                                                                                                                                                              м.н.;
                                                                                                                                                                                                                                                                     rat apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                        #text_change
                                                                                                                                                                                                                                                                                                                                                                                    Norway
                                                                                                                                                                                                                                                                                                              Johnson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytoplasmic
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

```
##molecule_type DNA
##residues 737-1031 ##label SEM
##cross references GB:M11767; NID:g182163; PID:g553282
REFERENCE A44188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
ENTRY
TITLE
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ENTRY
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.7%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                 #journal #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
#journal
#title
                                                                                                                                                                                                                                                                                                    #authors Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
#journal Proc. Natl. Acad. Sci. U.S.A. (1985) 82:6497-6501
#title A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in a human salivary adenocarcinoma.
#cross-references_MUID:86016729
#cross-references MUID:86070181
#accession A44188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #accession
                                                                                                                                                                       #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #cross-references_MUID:86118663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-1255 ##label YAM
##cross-references GB:X03363; NID:g31197; PID:g31198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL:AF003534; NID:g2738385; PID:g2738451
W #length 1186 #molecular-weight 138020 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues 1-1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c-erb-B-2 protein precursor; kinase-related transforming protein erbB2; v-erbB-related protein HER-2/neu #formal_name Homo sapiens #common_name man 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change
                                                                                                 Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; GraA.; McGrath, J.; Seeburg, P.H.; Libermann, T.A.; Schlessinger, J.; Francke, U.; Levinson, A.; Ullrich, Science (1985) 230:1132-1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba
Miyajima, N.; Saito, T.; Toyoshima, K.
Nature (1986) 319:230-234
Similarity of protein encoded by the human
epidermal growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strategy between insect and vertebrate iridoviruses T03180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T03180 #type complete
tyrostne protein kinase homolog - Chilo iridescent virus
#formal_name Chilo iridescent virus
24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes (1997) 15:235-245
The DNA sequence of Chilo iridescent virus between the
coordinates 0.101 and 0.391; similarities in coding
                                                                            Tyrosine kinase receptor with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A24571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A24571; A25491; A44188; B44188; I59509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A24571 #type complete
protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A24571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-1186 ##label BAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 2;
Pred. No. 1.64e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                            extensive homology to
                                                          location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nomura, N.;
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Gaps

0

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#note
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##molecule_type mRNA
##residues
##residues
##residues
##label COU2
##cross-references GB:M11730; NID:g183986
REFERENCE 159509
##ccession B44188
REFERENCE 259509
                                                                     SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references GB:L29395; NID:g459807; PID:g459808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-21
22-1255
Query Match 66.7%;
Best Local Similarity 45.5%;
                                                                                                             753
1139,1221,1222,
1248
                                                                                                                                                                                                                                                                                                                                       654-675
676-1255
                                                                                                                                                                                                       989
                                                                                                                                                                                                                                               726-734
68,124,187,259,530,
571,629
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70-304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal Mol. Cell. Biol. (1987) 7:2597-2601
#title Human HER2 (neu) promoter: evidence
for transcriptional initiation.
#cross-references MUID:87286898
#accession 157622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #map_position #introns
                                                                                                                                                                                                                                                                                                                     718-983
                                                                                                                                                                                                                                                                                                                                                                                                           395-605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #cross-references MUID:85272597
#accession I59509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 740-910 ##label COUI
##cross-references GB:M12036; NID:g183988; PID:g183989
#cession B44188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-191 ##label TAL
##cross-references GB:M16792; NID:g183983; PID:g553332
##CPSS-references GB:M16792; NID:g183983; PID:g553332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
##residues 832-909 ##label REX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.;
J.; Givol, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotransferase; proto-oncogene; receptor; transforming protein; transmembrane protein; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily epidermal growth factor receptor; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catalyzes the phosphorylation of a peptidyl tyrosine residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             King, C.R.; Kraus, M.H.; Aaronson, S.A. Science (1985) 229:974-976
Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
                                                              #length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 тотостоду
                                                                   #binding_site phosphate (Tyr) (covalent) (by
autophosphorylation) #status predicted
yth 1255 #molecular-weight 137909 #checksum
                                                                                                                                                  #domain transmembrane #status predicted #label TMM\
#domain intracellular #status predicted #label INT\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain EGF receptor extracellular domain repeat #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain signal sequence #status predicted #label SIG\
#product protein-tyrosine kinase erbB2 #status predic
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                        #domain EGF receptor extracellular domain repeat #label
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                                                              #molecular-weight 137909
Score 50; DB 1; L
Pred. No. 1.64e+01;
                       Length 1255,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for multiple mechanisms
                                                                   #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene occurs
                                                                   9382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted
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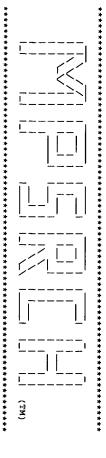
```
Matches 5; Conservative 5; Mismatches 1; Indels 0;

Db 63 TYLPTNASLSF 73

:||:|:||:
Qy 2 SYLSTSSSLDY 12
```

Search completed: Thu Sep Job time : 19 secs.

2 12:31:23 1999



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:31:39 1999; MasPar time 2.20 Seconds
154.507 Million cell updates/sec

Abular output not generated.

Title: >US-08-599-226-29
Description: (1-12) from USO8599226.pep
Perfect Score: 75
Sequence: 1 ASYLSTSSSLDY 12

Scoring table: PAM 150 Gap 15

earched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37.\_\_\_\_

abase: swiss-prot37.

Statistics: Mean 25.063; Variance 28.009; scale 0.895

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

asult No.	Score	% Query Match	Length	BB	ID	Description	Pred. No.
1	54	72.0	158	1	DHSD_BOVIN	SUCCINATE DEHYDROGENAS	9.05e-01
N	54	72.0	159	4سر	DHSD_HUMAN		9.05e-01
ω	52	•	917	ш	GLRK_LYMST		2.48e+00
4	51		1038	<b></b>	SOG_DROME	DORSAL-VENTRAL PATTERN	4.06e+00
ъ	50		626	ш	CEIB_ECOLI	COLICIN IB PROTEIN.	6.61e+00
σ	50		1255	$\vdash$	ERB2_HUMAN	ERBB-2 RECEPTOR PROTEI	6.61e+00
7	49	65.3	564	ш	5HT1_DROME	5-HYDROXYTRYPTAMINE RE	1.07e+01
œ	49		1469	ب	DP27_CAEEL	CHROMOSOME CONDENSATIO	1.07e+01
9	48		37	ب	YRYL_CAEEL	HYPOTHETICAL 4.1 KD PR	1.71e+01
10	48	64.0	272	Н	YIGL_HAEIN	HYPOTHETICAL PROTEIN H	1.71e+01
H	48	64.0	297	Н	PUR7_MYCLE	PHOSPHORIBOSYLAMINOIMI	1.71e+01
12	48	64.0	297	٢	PUR7_MYCTU	PHOSPHORIBOSYLAMINOIMI	1.71e+01
13	48	64.0	428	Н	B4AR_MELGA	BETA-4C ADRENERGIC REC	1.71e+01
14	48	64.0	441	۲	SECY_MYCTU	PREPROTEIN TRANSLOCASE	1.71e+01
15	48	64.0	475	$\vdash$	YM61_YEAST	HYPOTHETICAL 55.3 KD P	1.71e+01
16	48	64.0	505	ب	TUB_MOUSE	TUBBY PROTEIN.	1.71e+01
17	48	64.0	506	۳	TUB_HUMAN	TUBBY PROTEIN HOMOLOG.	1.71e+01
18	48		697	۳	TRP_SCHPO	TRYPTOPHAN SYNTHASE (E	1.71e+01
19	48	64.0	1211	1	ATH1_YEAST	VACUOLAR ACID TREHALAS	1.71e+01
20	47	•	330	_	ODBA_BACSU	2-OXOISOVALERATE DEHYD	2.71e+01
21	47		517	$\vdash$	DMPN_PSESP	PHENOL HYDROXYLASE P3	٠
22	47	62.7	579	_	YR47_CAEEL	HYPOTHETICAL 66.0 KD P	2.71e+01
23	47	62.7	626	,_	CEIA_ECOLI	COLICIN IA PROTEIN.	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	
46	46	46	46	46	46	46	46	46	46	46	46	46	46	47	47	47	47	47	47	47	4
61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	62.7	62.7	62.7	62.7	62.7	62.7	62.7	
653	577	509	471	471	471	464	442	352	196	171	167	132	127	1522	1294	963	963	848	780	687	001
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HYPOTHETICAL 75.9 KD P	CTP SYNTHASE 2 (EC 6.3	TYROSINE-PROTEIN KINAS	FLAVONOL 3-0-GLUCOSYLT	FLAVONOL 3-0-GLUCOSYLT	FLAVONOL 3-0-GLUCOSYLT	COLANIC ACID BIOSYNTHE	4-HYDROXYPHENYLPYRUVAT	HYPOTHETICAL 39.7 KD P	MYELIN BASIC PROTEIN (	MYELIN BASIC PROTEIN (	MYELIN BASIC PROTEIN (	HYPOTHETICAL 14.7 KD P	MYELIN BASIC PROTEIN S	HYPOTHETICAL 171.5 KD	HYPOTHETICAL 149.2 KD	IRON-RESPONSIVE ELEMEN	IRON-RESPONSIVE ELEMEN	AMINOPEPTIDASE N (EC 3	HYPOTHETICAL 88.2 KD P	VIBRIOBACTIN RECEPTOR	THE CHILD LAND CO. IN THE CO.
4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	4.26e+01	2.71e+01	2.71e+01	2.71e+01	2.71e+01	2.71e+01	2.71e+01	2.71e+01	***

# ALIGNMENTS

Вb	X m O	SO SO	88888888	366666668888888888888888888888888888888	RESULT ID DAC ODT TI DT TI TI DT TI
81 AAYLNPCSAMDY 92	Query Match 72.0%; Score 54; DB 1; Length 158; Best Local Similarity 50.0%; Pred. No. 9.05e-01; Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	CTRON TRANSPORT; HEME; TRANSMEMBRAN E.  MITOCHONDRION (POTENTIAL).  SUCCINATE DEHYDROGENASE [UBIQUINONE CYTOCHROME B SMALL SUBUNIT.  POTENTIAL.  POTENTIAL.  703D5238 CRC32;	SWISS-PROT entry is copyright. It is produced en the Swiss Institute of Bioinformatics and uropean Bioinformatics Institute. There are n by non-profit institutions as long as its cied and this statement is not removed. Usage ies requires a license agreement (See http://wndan email to license@isb-sib.ch).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SIEDNOY S.K., YU L., YU L.A.;  SHENOY S.K., YU L., YU L.A.;  SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.  -I- SUBUNIT: COMPOSED OF A 27 KD IRON PROTEIN (IP), A 70 KD  FLAVOPROTEIN (FP) AND A CYTOCHROME B COMPOSED OF TWO INTEGRAL  MEMBRANE PROTEINS.  -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  INNER MEMBRANE.	DHSD_BOVIN STANDARD; PRT; 158 AA.  Q95123; Q95123; 15-DEC-1998 (REL. 37, CREATED) 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE-UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) (QPS3).  SUBUNIT) (QPS3). SUBUNIT) (QPS3). BOS TAURUS (BOVINE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; EUKARYOTA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOS.

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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VEF
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O14521;
15-DEC-1998 (REL.
15-DEC-1998 (REL.
15-DEC-1998 (REL.
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HIRNAKE H., TANIWAKI M., KIJIMA S., KITA K.;

"Cytochrome b in human complex II (succinate-ubiquinone oxidoreductase): cDNA cloning of the components in liver mitochondria and chromosome assignment of the genes for the large (SDHC) and small (SDHD) subunits to 1q21 and 11q23.";

CYTOGENET. CELL GENET. 79:132-138(1997).

-i- SUBUNIT: COMPOSED OF A 27 KD IRON PROTEIN (IP), A 70 KD FLAVOPROTEIN (FP) AND A CYTOCHROME B COMPOSED OF TWO INTEGRAL
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SEQUENCE
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE-UBIQUINONE REDUCTASE MEMBRANE ANCHOR
                                    GLUTAMATE RECEPTOR PRECURSOR.
LYMNAEA STAGNALIS (GREAT POND
EUKARYOTA; METAZOA; MOLLUSCA;
                                                                        GLRK_LYMST STANDARD; PRT; 917 AA. P26591; P26591; O1-AUG-1992 (REL. 23, CREATED) O1-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE) O1-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest use by non-profit institutions as gas its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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Pred. No. 9.
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SUCCINATE DEHYDROGENASE [I
CYTOCHROME B SMALL SUBUNI:
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                                     GASTROPODA; PULMONATA;
                                                 SNAIL)
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                                     BASOMMATOPHORA;
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Best Local Similarity
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01-NOV-1997 (RE:
01-NOV-1997 (RE:
15-JUL-1998 (RE:
DORSAL-VENTRAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE: 92070466.
HUTTON M.L., HARVEY R.J., BARNARD E.A., "Cloning of a CDNA that encodes an inve
                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
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FEBS LETT. 292:111-114(1991).
SEQUENCE FROM N.A. MEDLINE; 95047398. FRANCOIS V., SOLLO
                                                     DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHI
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SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS
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S18443; S18443.
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  SOLLOWAY
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                                           DROSOPHILA.
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                                                   ARTHROPODA;
BRACHYCERA;
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54.5%;
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                                                     MUSCOMORPHA;
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No. 2.48e+00
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  EMERY J.,
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                                                               HEXAPODA;
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                                                                                             GASTRULATION PROTEIN).
                                                      EPHYDROIDEA;
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13-AUG-1987
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GENES DEV.
    SEQUENCE FROM N.A MEDLINE; 87008385
                                                                            ESCHERICHIA COLI.
PLASMID INCI1 COLIB-P9.
BACTERIA; PROTEOBACTERIA;
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TRANSMEMBRANE; DEVELOPMENTAL
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                                                                ESCHERICHIA.
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SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: ABUTS THE DORSAL DPP-EXPRESSING CELLS IN A
LATERAL STRIPE 14-16 CELLS WIDE. LATER IN EMBRYOGENESIS IT IS
EXPRESSED IN NEUROECTODERM AND IN THE ENDODERM SPACED ALONG THE
ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING GUT.
DEVELOPMENTAL STAGE: EMBRYOGENESIS.
SIMILARITY: TO XENOPUS DORSALIZING FACTOR CHORDIN.
SIMILARITY: CONTAINS 4 VWFC DOMAINS.
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llarity 60.0%;
Conservative
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Best Local S
Matches
                                                                                                                                                                  13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECU
(P185ERBB2) (NEU PROTO-ONCOGENE) (C-ERBB-2).
ERBB2 OR HER2 OR NGL OR NEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA and amino acid sequence analysis genes of colicins Ia and Ib.";
J. BACTERIOL. 168:228-236(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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NUCLEIC ACIDS RES. 12:8748-8748(1984).

-!- FUNCTION: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS

TRANSMEMBRANE TOXINS DEPOLARIZE THE CYTOPLASMIC MEMBRANE,

TO DISSIPATION OF CELLULAR ENERGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. BACTERIOL.
[2]
                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
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"Analysis of a cloned colicin Ib gene: complete
and implications for regulation of expression.";
NUCLEIC ACIDS RES. 12:6727-6739(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MANKOVICH J.A., LAI I "Organization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MANKOVICH J.A.,
   SEQUENCE FROM N.A
                                                                  PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                              ERB2_HUMAN
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PIR; D25035; D25035.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TE; PS00276; CHANNEL_COLICIN; PF01024; Colicin; 1. P06716; 1CII.
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X01009; G41142; -.

M13820; G144648; -.
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85014128.
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                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAI P.H., GOKUL f the colicin Ib
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                                                                      HOMINIDAE;
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Pred. No. 6.61e+00
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gene. Promoter
                                                                                                                                                                                                 KINASE PRECURSOR (C-ERBB-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promoter structure
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NP_BIND
BINDING
ACT_SITE
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MIM; 1648
PROSITE;
PROSITE;
PROSITE;
PFAM; PFO
PFAM; PFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEMBA K., KAMATA N., TOYOSHIMA K., YAMAMOTO T.;

"A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in human salivary gland adenocarcinoma.";

PROC. NATL. ACAD. SCI. U.S.A. 82:6497-6501(1985).

-I-FUNCTION: NEUREGULINS AND G930 ARE POTENTIAL LIGANDS FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN.

-I-CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

-I-SUBCILIULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I-SUBCILIULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAITO T., TOYOSHIMA K.; "Similarity of protein encoded by the human epidermal growth factor receptor."; NATURE 319:230-234(1986).
                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 860
COUSSENS L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 737-1031 FROM N.A. MEDLINE; 86016729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shares chromosomal location with neu oncogene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCGRATH J., SEEBURG P.H., LIBERMANN T.A., SCHLESSI FRANCKE U., LEVINSON A., ULLRICH A.; "Tyrosine kinase receptor with extensive homology".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                       DOMAIN
                                                                              DOMAIN
                                                                                                     SIGNAL
                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCIENCE 230:1132-1139(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 86118663.
YAMAMOTO T., IKAWA S
SAITO T., TOYOSHIMA
                                                                                                                  RANSFERASE;
                                                                                                                                         SITE: PS00107; PROTEIN_KINASE_ATP; 1
SITE: PS00109; PROTEIN_KINASE_TYR: 1
SITE: PS50011; PROTEIN_KINASE_DOM; 1
M; PF00069; pkinase; 1.
M; PF00757; Furin-like; 1.
M; PF001030; Recep_L_domain; 2.
P; P11362; 1FGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESIDUES (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON
                                                                                                                                                                                                                                164870;
                                                                                                                                                                                                                                           A24571; A24571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86070181.
L., YANG-FENG T.L.,
   653
676
720
726
753
                                                                                                               TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKAWA S.,
                                                                                                                               GLYCOPROTEIN;
   1255
652
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753
845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .., LIAO Y.C., CI
LIBERMANN T.A.,
 CYTOPLASMIC (POTENTIA PROTEIN KINASE. ATP (BY SIMILARITY). ATP (BY SIMILARITY). BY SIMILARITY).
                                                                                                                              MULTIGENE
                                                               POTENTIAL.
                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                        ERBB2 PROTEIN.
                                                                                                     POTENTIAL.
                                                                                                                 KINASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEMBA K., NOMURA N., MIYAJIMA N.,
                                                                                                                 ATP-BINDING;
                                                                                                                             FAMILY; RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEN E., GRAY !
                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c-erb-B-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to EGF receptor
                                                                                                                 PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R J.,
                                                                                                                              SIGNAL
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CONFLICT
CONFLICT
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CARBOHYD
CARBOHYD
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MOD_RES
CARBOHYD
 TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5HT1
                                 TRANSMEM
DOMAIN
                                                                                      FLYBASE; PROSITE;
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      "Cloning and characterization activates adenylate cyclase.", PROC. NATL. ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRAC
PTERYGOTA; DIPTERA; BRACHYCERA; MUSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
5-HYDROXYTKYPTAMINE RECEPTOR 1 (5-HT RECEPT
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=OREGON-R; : MEDLINE; 91062395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5HT-R1 OR 5-HT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                 G-PROTEIN
                                                                                                           PIR; A38271; A38271.
GCRDB; GCR_0023; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P20905
                                                                                                                                 EMBL; M55533; G156725;
                                                        TRANSMEM
                                                                            PFAM; PF00001;
                                                                                                                                                                                                                                                                                                                                                                          WITZ P.,
                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: HEAD.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                            C. NATL. ACAD. SCI. U.S.A. 87:8940-8944(1990).

FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERNY RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION AS A NEUROTRANSMITTER, A HORMONE, AND A MITGGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
                                                                                                                                                                                                                                        BUT WITH ONE EXTRA POTENTIAL TRANSMEMBRANE DOMAIN.
                                                                                                                                                                                                                                                                                     CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 66.7%;
Similarity 45.5%;
                                                                                      FBgn0004573; 5-HT7.
PS00237; G_PROTEIN_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                      AMLAIKY N., PLASSAT J.-L.,
                                                                  COUPLED
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1248
1248
1248
124
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189
199
223
237
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-R; TISSUE-HEAD;
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1248
68
124
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530
571
629
1170
                                                                   RECEPTOR;
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198
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236
258
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Pred.
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0 (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (
3 (POTENTIAL).
                                                                 TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRACHEATA; HEXAPODA; INSECTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; DB 1; 1
No. 6.61e+00
                                                                                                                                                                                                                                                                                                                                                             , MAROTEAUX L., BORREI Drosophila serotonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REF. 2).
REF. 2).
CRC32;
                                 (POTENTIAL)
                                                                 GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                        EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SEROTONIN RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                      BORRELLI E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                             receptor
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DISULFID
SEQUENCE
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TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                      This SWI
                                        EMBL; L35274; G529385; -. EMBL; Z35602; E1348662; -. WORMPEP; R13G10.1; CE0105
                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                       CHROMOSOME EXPRESSION.

-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYOS AND EARLY-STAGED LARVAE.
-!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
-!- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: ACTS TO REDUCE EXPRESSION OF BOTH HERMAPHRODITE X CHROMOSOMES. DPY-27 BECOMES SPECIFICALLY LOCALIZED TO THE X CHROMOSOMES OF WILD-TYPE XX EMBRYOS, BUT REMAINS DIFFUSELY DISTRIBUTED THROUGHOUT THE NUCLEI OF MALE (XO) EMBRYOS. COUI IMPLEMENTS DOSAGE COMPENSATION BY CONDENSING THE CHROMATIN STRUCTURE OF X IN A MANNER THAT CAUSES GENERAL REDUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GARDINER A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITI/
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (REL. 33, CI
01-FEB-1996 (REL. 33, LI
01-NOV-1997 (REL. 35, LI
CHROMOSOME CONDENSATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans dosage compensation
chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPY-27 OR R13G10.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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  ATP-BINDING; COILED NP_BIND 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DPY-27:a chromosome condensation protein homolog that regulates elegans dosage compensation through association with the {\bf x}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95042743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.-T., ALBERTSON D.G., MEYER B.J.;
                                                                                                                                   s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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564
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60861
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35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33, CREATED)
                                             CE01052
129
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NUCLEAR PROTEIN.
ATP (POTENTIAL).
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4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 1; I
Pred. No. 1.07e+01;
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
9 X 2 AA TANDEM REPEATS O
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Y SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHABDITIA;
                                                                                                                                                         http://www.isb-sib.ch/announce/
                                                                                                                                                                                   Usage
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WORMPEP; FU,...
HYPOTHETICAL PROTEI
TOTRINGE 37 AA;
                                                                                                                                              YIGL_HAEIN
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                                          HAEMOPHILUS
                                                            HAEMOPHILUS
BACTERIA; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z68314; E1345182; -. WORMPEP; F07H5.4; CE09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-BRISTOL N2;
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                                                            PROTEOBACTERIA;
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; RHABDITOIDEA;
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L 4.1 KD PROTEIN F07H5.4 IN CHROMOSOME II.
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, PROTEIN HI0597.
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Pred. No. 1.71e+01
2; Mismatches
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5; Mismatches 1
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K->I: LOSS OF FUNCTION.
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COILED COIL (POTENTIAL).
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                                                              SUBDIVISION; PASTEURELLACEAE;
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                                                                                                                                                                    UPDATE
                                                                                                                                                                                                                                  272
                                                                                                                                              UPDATE)
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            This SWISS-PROT entry is copyright. It is produced through a col between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restrictic use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.ch
                                                                                                                                    PUR7_MYCLE 008361;
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KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.
MCKENNEY K., SUTTON G., FITZHIGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                MYCOBACTERIUM LEPRAE.
BACTERIA; FIRMICUTES;
ACTINOMYCETALES; CORYN
                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE
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SCIENCE 269:496-512(1995).

SSINILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL.
(B.SUBTILIS) FAMILY. STRONG, TO E.COLI YIGL.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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FLEISCHMANN R.D.,
                                                                                                                                                                                                                                                    BADCOCK K.,
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SEQUENCE 272 AA; 3
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58.3%;
license agreement (See http://www.isb-sib.ch/announce/license@isb-sib.ch).
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                                                                                                                                                                                                                                                   С.м.,
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Pred. No. 1.71e+01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
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                                                                                                                                                                                                                                                   BARRELL
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                                                           restrictions
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                                                                             EMBL outstation
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                                                                                                                                                  EMBL; Z80226; E266570; -.

EMBL; Z80226; E266570; -.

EMBL; U34957; G1144522; -.

PROSITE; PS01057; SAICAR_SYNTHETASE_1;

PROSITE; PS01058; SAICAR_SYNT; 1.

PFAM; PF01259; SAICAR_SYNT; 1.

PFAM; PF01259; SAICAR_SYNT; 1.
                                                                                                 CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCLEAN J., HARRIS D., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DOBJ DATA BANKS
-I- CATALYTIC ACTIVITY: ATP + 1- (5-PHOSPHORIBOSY)-4-CARBOXY-5-
AMINOIMIDAZOLE + L-ASPARTATE - ADP + ORTHOPHOSPHATE + 1- (5-
PHOSPHORIBOSYL)-4- (N-SUCCINO-CARBOXAMIDE)-5-AMINOIMIDAZOLE.
-I- PARHMAY: SEVENTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
-I- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
-I- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q59566; P77904;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE
                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JACKSON M., BERTHET F.-X., OTAL GICQUEL B., GUILHOT C.;
"The Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYCOBACTERIUM TUBERCULOSIS.

BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAICAR SYNTHETASE).
PURC OR MTCY369.24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 295151; E315054; -.
PROSITE; PS01057; SAICAR_SYNTHETASE_1;
PROSITE; PS01058; SAICAR_SYNT; 1.
PFAM; PF01259; SAICAR_SYNT; 1.
                                                                                                                                                PURINE BIOSYNTHESIS;
CONFLICT 124 1:
                                                                                                                                                                                                                                                                                                                                                                                          modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MICROBIOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolation and characterization of MICROBIOLOGY 142:2439-2447(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EME EMERGE BUTCHER BIOINFORMATICS Institute. There are no restrict by non-profit institutions as long as its content if the and this statement is not removed. Usage by and the statement is not removed.
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Similarity 54.5%;
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  Similarity 54.5% 6; Conservative
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32930 MW;
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                        64.0%;
54.5%;
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                      Score 48; DB 1;
Pred. No. 1.71e+01
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Pred. No. 1.71e+01
3; Mismatches
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  Mismatches
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                                                                                              REF. 1
CRC32;
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                                            Length 297;
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MBL outstation -
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HSSP; P07700; 1DEP.
G-PROTEIN COUPLED BY
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01-NOV-1995
                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                            EMBL; Ul3
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. BIOL. CHEM. 269:24810-24819(1994)
-!- FUNCTION: BETA-ADRENERGIC RECEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MELEAGRIS GALLOPAVO (COMMON TURKEY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; MELEAGRIDIDAE; MELEAGRIS.
                                                                                              DISULFID
LIPID
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                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: BROAD TISSUE DISTRIBUTION.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEN X.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 95014249.
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                      122
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                     YLAITAPLQY 131
  YLSTSSSLDY
                                                                                                                                                                                                                                                                                                                                         U13977; G556604; -.
U13978; G555882; -.
U13978; G_PROTEIN_RECEPTOR;
                                          Similarity 40.0% 4; Conservative
                                                                                                                                                                                                                                                                                                   FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REL.
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                                                                                                                                       Bioinformatics Institute. The profit institutions as long
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32, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDAT
C RECEPTOR.
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164
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211
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261
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428
                                                  64.0%;
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                                        Score 48;
Pred. No.
5; Misma
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POTENTIAL.
BY SIMILAR
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PALMITATE (BY SIN
8B794F0C CRC32;
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5 (POTENTIAL)
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2 (POTENTIAL)
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6 (POTENTIA
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1.71e+01;
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P94926;
15-JUL-1998
15-JUL-1998
15-DEC-1998
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MEDLINE: 98295987.

COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS GORDON S.V., EIGLMEEIER K., GAS S., BARRY C.E. III, TEKAIA F., GORDON S.V., EASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S. HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., OLIVER S., OSBORNE J., QUALI M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J. TAYLOR K., WHITEHBAD S., BARRELL B.G.;
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                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-i- FUNCTION: INVOLVED IN PROTEIN EXPORT, INTERACTS WITH SECA TO ALLOW THE TRANSLOCATION OF ENTOREIN ACROSS THE PLASMA MEY FORMING PART OF A CHANNEL (BY SIMILARITY).

-i- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) TO COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; NATURE 393:537-544(1998).
                                                                                                                                                                                                                                                                                   PROSITE; PS00755;
                                                                                                                                                                                                                                                                                                                EMBL; AL021958; E1253270; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SPECIES=M.BOVIS; STRAIN=BCG;
KIM J.K., CHOE Y.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOBACTERIUM TUBERCULOSIS, AND MYCOBACTERIUM BOVIS. BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECY OR RV0732 OR MTV041.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UI
15-DEC-1998 (REL. 37, LAST ANNOTATION
PREPROTEIN TRANSLOCASE SECY SUBUNIT.
                                                                                                                                                                                                                                         PROTEIN
                                                                                                                                                                                                                                                       PFAM; PF00344;
                                                                                                                                                                                                                                                                      PROSITE;
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             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
Similarity 50.0% 6; Conservative
                                                                                                                                                                                                                                         TRANSPORT;
                                                                                                                                                                                                                                                                   PS00756; SECY_2;
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157
180
215
272
318
382
                                                                                                                                                                                                                                                       secY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                   SECY_1;
                                                                                        144
177
200
235
235
338
402
                                                                                                                                                                                                                                         TRANSMEMBRANE;
             64.0%;
50.0%;
                                                            47611
                                                           WW.
            Score 48; DB 1;
Pred. No. 1.71e+01
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                                                           26ElFAC6 CRC32;
Mismatches
                                                                                                                                                                                                                                       TRANSLOCATION
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                          Length 441;
Indels
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Gaps
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ASYLSTSSSLDY 12

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                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.0%;
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YM61_YEAST STANDARD; PRT; 475 AA.

(03652;
(01-NOV-1997 (REL. 35, CREATED)
(01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
(01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(11-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(11-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(12-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(13-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(13-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(13-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(14-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(15-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
(15-NOV-1997 (REL. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEDMAN K., BROWN D., WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z49809; G854463; -.
PFAM; PF00091; tubulin; 1.
HYPOTHETICAL PROTEIN.
SEQUENCE 475 AA; 55312 MW;
                                                                                                                                                                                                                                                                                                                                                                                    321 YLTTAITLGY 330
                                                                                                                                                                                                                                                            3 YLSTSSSLDY 12
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                                                                         2 12:31:47 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 1; Length 475; Pred. No. 1.71e+01; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18FA4F03 CRC32;
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[ME]

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm on:

on: Thu Sep 2 12:32:06 1999; MasPar time 4.45 Seconds 147.067 Million cell updates/secondar output not generated.

Title: VUS-08-599-226-29
Description: (1-12) from US08599226.pep
Perfect Score: 75
Sequence: 1 ASYLSTSSSLDY 12

Scoring table: PAM 150 Gap 15

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

sptrembl9
T:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_bhage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 24.003; Variance 31.514; scale 0.762

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

sult No.	Score	% Query Match	Length	BB	ID	Description	Pred. No.
<b>J</b>	55	73.3	649	ω	060167	PROTEIN COMPLEX ASSEMB	2.58e+00
ν	54	72.0	349	G	017959	PROTEIN.	
ω	54	72.0	503	ν	026074	٠	4.07e+00
4	53	70.7		14	011696	NUCLEOPROTEIN (FRAGMEN	•
υ	53	70.7		σ	Q25144		
σ	53	70.7	897	5	Q17336	LET 858.	6.38e+00
7	53	70.7		υ	061198	F15E6.6 PROTEIN.	6.38e+00
æ	52	69.3		υ	P91143	SIMILAR TO ACETYLTRANS	9.96e+00
9	52	69.3		13	093514	AXIAL PROTOCADHERIN (F	9.96e+00
10	52	69.3		5	001623	₽.	9.96e+00
11	51	68.0		9	048385	ORF83.	1.55e+01
12	51	ω.		10	023552	HYPOTHETICAL 52.8 KD P	1.55e+01
13	51	•	582	ω	074931	ALTERNATIVE NADH-DEHYD	1.55e+01
14	51	68.0	1035	13	057537	NF-PROTOCADHERIN.	1.55e+01
15	51	68.0	1069	11	088185	BH-PROTOCADHERIN-A.	1.55e+01
16	51	68.0	1069	4	060245	PCDH7 (BH-PCDH)A.	1.55e+01
17	51	68.0	1072	4	060246	PCDH7 (BH-PCDH)B.	1.55e+01
18	51	68.0	1200	4	060247	PCDH7 (BH-PCDH)C.	1.55e+01
19	50	66.7	293	Ν	051095	CONSERVED HYPOTHETICAL	2.38e+01
20	50	66.7	444	u	P91141	SIMILAR TO ACETYLTRANS	2.38e+01

45	44	43	42	41	40	39	38	37	36	35	34	S S	32	31	30	29	28	27	26	25	24	23	22	7.7
48	48	48	48	48	48	48	48	49	49	49	49	49	49	49	49	49	49	50	50	50	50	50	50	50
64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	65.3		65.3		•			•	•		66.7	٠	٠	٠	66.7	•	66./
1685	966	954	505	438	420	325	170	1406	1026	650	409	392	384	377	222	204	112	1186	989	626	626	626	626	469
10	H	N	11	N	w	N	N	4	4								ω	14	11	N	N	N	N	N
004142	055098	084594	808880	067997	P78765	Q55392	086052	015082	Q08174	050417	025853	050873	Q11197	084397	P70023	Q12097	Q07255	055767	Q63052	Q46740	Q46738	Q46734	046732	032204
н	SERINE/THREONINE KINAS	HYPOTHETICAL 109.2 KD	TUBBY PROTEIN.	AMTB.	FISSION YEAST (FRAGMEN	HYPOTHETICAL 35.4 KD P	AMMONIUM TRANSPORTER (	KIAA0377.	PROTOCADHERIN 42 PRECU	MULTI-FUNCTIONAL ENZYM	NADH-UBIQUINONE OXIDOR	CONSERVED HYPOTHETICAL	HYPOTHETICAL 41.9 KD P	HYPOTHETICAL 41.4 KD P	OLFACTORY RECEPTOR (FR	HYPOTHETICAL 22.6 KD P		PUTATIVE TYROSINE PROT	APOLIPOPROTEIN B (FRAG	COLICIN PROTEIN.	COLICIN PROTEIN.	COLICIN PROTEIN.	COLICIN PROTEIN.	YVSH PROTEIN.
5.57e+01				5.57e+01		•		3.65e+01										2.38e+01				2.38e+01	2.38e+01	2.38e+0

# ALIGNMENTS

RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; [1] SEQUENCE FROM N.A. LLOYD C.; SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS	MOIBZ.5.  KOIBZ.5.  KOENORHABDITIS ELEGANS.  CAENORHABDITIS ELEGANS.  EUKARYOTA: METAZOA: NEMATODA: SECERNENTEA: RHARDITIA:	DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE) DF M0182 5 DROWETH	01-JAN-1998 (TREMBLREL. 05, CREAT	ID 017959 PRELIMINARY; PRT; 349 AA. AC 017959;	RESULT 2	Qy 2 SYLSTSSSLDY 12	Db 234 NYLSTARSLEF 244	Query Match 73.3%; Score 55; DB 3; Length 6 Best Local Similarity 54.5%; Pred. No. 2.58e+00; Matches 6; Conservative 4; Mismatches 1; Inde	SEQUENCE 649 AA; 72985 M	. BECK A., REINHARDT R., WOOD V., RAJANDREAM M.A., SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDRJ DATA RA	STRAIN=972H-;	RP SEQUENCE FROM N.A.	SCHIZOSACCHAROMYCES.	OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;	GN SPBC19F8.03C.	01-AUG-1998 (TREMBLREL. 07, LAST	01-AUG-1998 (TREMBLREL. 07,	AC O60167; PRELIMINARY; PRT; 649 AA.	SULT 1
CA	RDITIA: RHARDITIDA:	TE) DATE)						Length 649; ; 1; Indels 0; Gaps 0;		., BARRELL B.G.;				ŋ A ŋ ,		DATE)	TE)		

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RESULT
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AC 01
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Best Loc
Matches
   O11696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the gastric pathogen Helicobacter pylori[published erratum appears in Nature 1997 Sep 25;389(6649):412].";
NATURE 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOMB J. F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-F., GILL S., DOUGHERTY B.A NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCAYNE J.D., UTIERBACK T.R., PETERSON J.D., KELLEY J.M. COTTON M.D., WELIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
PROTEIN-EXPORT MEMBRANE
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026074;
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BACTERIA; PROTEOBACT
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EMBL; Z83116; E1348127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000652; G2314730;
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                                                                                                                                                                                                                                                                                                Similarity 60.0% 6; Conservative
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PROTEOBACTERIA; EPSILON SUBDIVISION;
                                                                                                                                                                                                                                                                                                                                                                                                                                 503 AA;
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                                     PRELIMINARY;
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. 05, LAST SEQUENC
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E PROTEIN (SECD).
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LAST ANNOTATION UPDAT
                                     PRT;
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1. No. 4.07e+00;
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1. No. 4.07e+00;
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                                                                                                                                                                                                                                                                                                    Indels
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FERRITARY OF THE RESULT OF THE
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Best Loc
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                                                                                     017336
Q17336;
Q17336;
Q1-NOV-1996
Q1-NOV-1996
Q1-JAN-1999
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025144;
025144;
01-NOV-1996
01-NOV-1998
01-NOV-1998
                               LET 858.
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01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1997 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NUCLEOPROTEIN (FRAGMENT).
MEASLES VIRUS (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).
VIRUSES; SERNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; MORBILLIVIRUS.
CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00027; HOMEOBOX_1; 1.

PFAM; PF00046; homeobox; 1.

HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN.

SEQUENCE 265 AA; 29579 MW; B68A753D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS LETT. 411:119-122(1997).
-i- SUBCELLULAR LOCATION: NUCLEAR EMBL; X/5217; G407415; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differentially expressed
metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A Mox homeobox gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HALIOTIS RUFESCENS (CALIFORNIA RED ABALONE).
EUKARYOTA; METAZOA; MOLLUSCA; GASTROPODA; PF
ARCHAEOGASTROPODA; HALIOTIDAE; HALIOTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of three lineages sequence analysis of N, P, M, F, a J. MED. VIROL. 52:113-120(1997). EMBL: D87487; D1020995; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  81 GSYLSMSSSKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 AAYLPTSTPLD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                      1 ASYLSTSSSLDY
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                                                               858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 75.0% 9; Conservative
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                                                                                     (TREMBLREL. (TREMBLREL. (TREMBLREL. (
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(TREMBLREL.
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llarity 63.6%;
Conservative
                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.7%;
75.0%;
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13950 MW;
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LAST SEQUENT ANNOTATION AND LAST ANNOTATION AND LAST AND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENTENANY G., MORSE D.E.;
gastropod mollusc Haliotis
ring larval morphogenesis ar
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Pred. No. 6.38e+00;
4; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53; DB 5; 1
Pred. No. 6.38e+00
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                                                                                                                                                                                                                 PRT;
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and
                                                                                                                     SEQUENCE UPDATE)
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                                                                                        ANNOTATION
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L genes in Japan.";
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                                                                                        UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 265;
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DT 01-AUG-
DT 01-AUG-
DT 01-E56.6
GN F15E6.6
OS CAENORH
OC EUKARYC
OC RHABDIT
RN [1]
RP SEQUENC
RC STRAIN-
RA WILSON
RA GARDNEI
RA GARDNEI
RA JONES A
RA PARSONE
RA SMALDOI
RA SMALD
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., CC
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNS
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGH
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHO
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VANGHAN K., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide semience from chi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998
01-AUG-1998
01-NOV-1998
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EMBL; U19615; G987227; -
EMBL; Z81525; E1351661;
SEQUENCE 897 AA; 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-N2 (BRISTOL);
KELLY W.G., COLES L.H.,
                                                                                                                                                                                                    SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ EMBL; AF038614; G2702437;
                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
MILLER N., STELLYES L.,
SUBMITTED (DEC-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
MEDLINE; 94150718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHABDITINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F15E6.6 PROTEIN.
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                                                                                                                                     PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
IRON-SULFUR.
SEQUENCE 1238 AA; 135726 MW; 9408B
                                                                                                                                                                                                                                                        WATERSTON R.;
                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLSTSSSLDY
YLETQSSLNY 711
                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TREMBLREL.)
(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHABDITOIDEA;
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larity 70.0%;
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                                        70.7%;
llarity 70.0%;
Conservative
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08,
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                                                                                                                                                                                                                                                                                                                                              BRADSHAW H., KEPPLER D.;
EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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Pred.
                                             Pred.
                                                                  Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                             Mismatches 2;
                                                                                                                                        9408BB7C
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No. 6.38e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1238
                                                                                          DB 5;
                                                                                                                                        CRC32;
                                                                                                                                                                                                                                   DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                      Length 1238;
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'CALLAGHAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FULTON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHOWNKEEN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COULSON
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RESULT 8

ID 991143;
AC 991143;
AC 991143;
DT 01-MAY-1997
DT 01-MAY-1997
DT 01-MOV-1998
DE SIMILAR TO AGE
GN C37H5.2.
OS CAENORHABDIT
OC EUKARYOTA; M
OC RHABDITINA; M
OC RHABDITINA; M
OC STRAIN-BRIST
RN [1]
RA HILSON R., A
RA BONFIELD J.,
RA CRAXTON N.,
RA CRAXTON N.,
RA CRAXTON N.,
RA CRAXTON N.,
RA CRAXTON S.,
RA GARDNER A.,
RA GARDRER A.,
RA GARDNER A.,
RA GARDNER A.,
RA GARDNER A.,
RA GARDNER A.,
RA GARD
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    FT RAPACTOR REPORTED TO THE REPORT OF THE RE
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Best Local Similarity
Matches 7; Conser
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093514;
093514;
01-NOV-1998
01-NOV-1998
01-NOV-1998
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROPPRA A., SAUNDERS D., SHOWNKEEN SMALDON N., SMITH A., SOUNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
AXIAL PROTOCADHERIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFERASE.
372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; U88315; G1825777; -.
PFAM; PF00561; abhydrolase; 1.
TRANCEFRACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAENORHABDITIS ELEGANS EUKARYOTA; METAZOA; NEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
DAVIDSON S., GILLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHABDITINA; RHABDITOIDEA;
                            YAMAMOTO A., DEROBERTIS E.M.; "Xenopus axial protocadherin."; "Xenopus axial protocadherin."; SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AF053469; G3598688; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94150718.
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                                                                                                                                                                                                                                                                XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NATURE 368:32-38(1994).
NON_TER
                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ASYLSTSSSLDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TREMBLREL.
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58.3%;
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03, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW;
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Pred. No. 9.
3; Mismatc
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CAENORHABDITIS.
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Best Local S
Matches
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Best Local :
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001623

001623;

01-JUL-1997 (TREMBLREL C

01-JUL-1997 (TREMBLREL C

01-JUL-1998 (TREMBLREL C

01-NOV-1998 (TREMBLREL C
                                           048385;
01-JUN-1998
01-JUN-1998
01-NOV-1998
       ORF83.
STREPTOCOCCUS THERMOPHILUS
                                                                                      CT 11
048385
                                                                                                                                                                                                                                                                                                                                                                                         WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SWALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MURRAY J.;
                                                                                                                                                                                                                                                                                                                                                                            WATSON A., WELLING.
"2.2 Mb of contiguous
"2.7 mng.";
                                                                                                                                                                                                                          SUBMITTED (APR-1997) TO 1
EMBL; U97007; G1938466;
PFAM; PF00060; lig_chan;
SEQUENCE 932 AA; 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2 MEDLINE; 94150718
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                 SUBMITTED (APR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                          Local Similarity
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                                                                                                                                                       AYLMESTSLEY 763
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475 i
                                        (TREMBLREL.) (TREMBLREL.)
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52268
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04, LA
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IONIC
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                                                                                                                                                                                                                                                                                                                 EMBL/GENBANK/DDBJ
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         BACTERIOPHAGE TP-J34.
RNA STAGE; TAILED PHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
IC CHANNEL PROTEINS.
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Pred.
3; M
                                       CREATED)
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9.96e+00;
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                                                                                                                                                                                         DB 5; L
9.96e+00;
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                                           UPDATE)
          PHAGES;
                                                                                                                                                                                                   Length 932;
                                                                                                                                                                              2;
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          SIPHOVIRIDAE
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RESULTATION OF THE PROPERTY OF
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Best Local S
Matches
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O23552;
O23552;
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDALL,
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
HYPOTHETICAL 52.8 KD PROTEIN.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EURARYOTA; VIRIDITLANNAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EURARYOTA; VIRIDITLANNAE; STREPTOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-TP-J34;
MEDLINE; 98122991.
MEDLINE; 98122991.
NEVE H., ZENZ K.I., DESIERE F., KOCH A., HELLER K.J., BRUSSOW H.;
"Comparison of the lysogeny modules from the temperate Streptococcus thermophilus bacteriophages TP-J34 and Sf121: implications for the thermophilus bacteriophage evolution.";
                                                                                                                                                                             LT 13
O74931
PRELIMINARY; PRT; 582 AA.
O74931;
O1-NOV-1998 (TREMBLREL. 08, CREATED)
O1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ALTERNATIVE NADH-DEHYDROGENASE PRECURSOR (EC 1.6.5.3)
(NADH DEHYDROGENASE (UBIQUINONE)) (UBIQUINONE REDUCTASE)
(TYPE I DEHYDROGENASE) (COMPLEX I DEHYDROGENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KREIS M., KAVANAGH T., MURPHY G., WAMBUTT R., POHL T PUIGDOMENECH P., HATZOPOULOS P., OBERMAIER B., DUESTE JONES J., PALME K., ANSORGE W., DELSENY M., BANCROFT SCHUELLER C., CHALMATZIS N.; SUBMITTED (JUL-1997) TO PURT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
BEVAN M., STIEKEMA W.,
KREIS M., KAVANAGH T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ
EMBL; 297342; E327038; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modular theory of phage evolutions of the virology 241:61-72(1998).
EMBL; AF020798; G2897100; -.
SEQUENCE 83 AA; 9876 MW;
                      SEQUENCE FROM
STRAIN-E150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                               DIPODASCACEAE;
                                                                                                                      ARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AGYLTSSSDLD 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 YLETSAFLEY 80
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larity 63.6%;
Conservative
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BRANDT U.;
                                                                                               YARROWIA.
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Pred. No.
2; Misma
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Pred.
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                                                                                                                      HEMIASCOMYCETES;
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1.55e+01;
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                                                                                                                      SACCHAROMYCETALES
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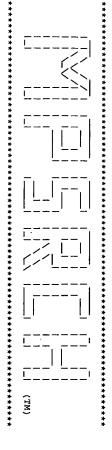
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SER BROCCE REPROCE OF THE PROCESS OF
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TRANSPORT REPORT OF THE PROPERTY OF THE PROPER
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Matches
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Best Local Similarity
Matches 6; Conser
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O88185;
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01-NOV-1998
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01-JUN-1998
01-JUN-1998
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SEQUENCE
                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 98277460.
MEDLINE; 98277460.
YOSHIDA K., YOSHITOMO-NAKAGAWA K., SEKI N., SASAKI M., SUGANO S.;
"Cloning, expression analysis, and chromosomal localization of
BH-protocadherin (PCDH7), a novel member of the cadherin
superfamily.";
                                                                                                                                                                                                                                                                                                                                                            MUS. MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of the YLNDH2 Gene Encoding the Alternative NADH: Ubiquinone Oxidoreductase from Yarrowia lipolytica."; SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
-!- COFACTOR: FAD; IRON-SULFUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH-PROTOCADHERIN-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
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XENOPUS LAEVIS (AFRICAN CLAWED FROG).
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SUGANO
                       SEQUENCE FROM N.A.
                                                                                                                       JENOMICS
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3 YLSTSSSLDY 12
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                                                                                                                       49:458-461(1998).
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582 AA;
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3 (TREMBLREL.
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54.5%;
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                          WATANABE
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808,
808,
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 13;
Pred. No. 1.55e+01;
3; Mismatches 1
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.55e+01;
3; Mismatches 2
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ALTERNATIVE NADH-DEHYDROGENASE.
, 0460C796 CRC32;
                          3
                          YAMAGUCHI
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                          TATEYAMA
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SERBER
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                           밁
                                                    Query Match
Best Local S
Matches
                                                                                                                   "cDNA cloning and chromosomal mapping of mouse BH-protocadherin.";
DNA SEQ. 0:0-0(1998).
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AB006758; D1033562; -.
PROSITE; PS00232; CADHERIN; 5.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT.
                                                                                                          SEQUENCE
                           486 FLHTSAPLDY 495
                                                    Local Similarity
nes 6; Conser
3 YLSTSSELDY
                                                                                                        1069 AA;
                                                   68.0%;
larity 60.0%;
Conservative
  12
                                                                                                        116314
                                                                                                       MW;
                                                    Score 51; DB 11;
Pred. No. 1.55e+01;
3; Mismatches 1
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Search completed: Thu Sep 2 12:32:56 1999 Job time: 50 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 12:34:45 1999; MasPar time 3.53 Seconds 72.272 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Title: Sequence: >US-08-599-226-30 (1-12) from USUS599226.pep 69 1 ASYLSTSSSLDD 12

Scoring table: PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

argeneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
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Statistics: Mean 16.937; Variance 50.990; scale 0.332

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Result No.
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W27589 W27586 W27587 W27587 W27594 W27593 W27563 W27592 W27591 W27591 W27591 W27591 W27591 W27591 W27591 W27591 W27591	ĬĎ
Anti-TNF-alpha antibo Canine IgE heavy chai T7 gene 10 leader seq M. tubbcrculosis ORF 2 PRRSV isolate 14/96 n	Description
7.15e-01 3.59e+00 3.52e+00 3.52e+00 7.70e+00 7.70e+00 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.24e+02 1.24e+02 1.24e+02	Pred. No.

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spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

RESULT 1  W27589 st AC W27589; AC W27589; DT 19-MAR-15 AT1-TNF KW Human; tt KW Heavy che KW cardiac c KW bone res KW bone res KW bone res KW bone res KW human umb OS Homo sapp PN W0972913 PD 14-AUG-11 PF 10-FEB-11 PF 10-FEB-11 PF 09-FEB-11 PF 09-FEB-11 PF 10-FEB-11 CC Talpha affif PT TNF alpha PS Claim 20 CC The press CC factor-al CC less and CC less and CC 1929 asse CC inhibits CC autoimut	44444333333322221117 4444433333332227652221198 5443765243321
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representations of the control of th	W81867 W62322 W33747 W40904 W47952 W430202 W440539 W30206 W32321 W62321 W62322 W37550 W37550 W37550 W37550 W37552 W48595 R48595 R48595 R48594 R48594 R48594 R48592 W41641 W62007 W41641 W86007
3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3	Human tumour suppress Pseudomonas fluoresce Pseudomonas gafa elem Amino acid sequence o ORF5 protein (gafa). ORF 5 protein encoded by Protein encoded by OR Ile 182 ORF 5 protein encoded by OR Ile 182 ORF 5 protein eseudomonas fluoresce Amino acid sequence o Pseudomonas fluoresce MBP-1.1 (11-29). Human myelin basic pr Human myelin basic pr Human myelin basic protein basic pr Human MBP-1.2 (11-31). Rat myelin basic protein basic protein basic protein basic protein myelin basic protein encoded by cluman Myelin basic protein encoded by cluman protein encoded the fluman encoded the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Hallen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; PJ Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; PJ Salfeld JG, Schoenhaut D, Vaughan TMF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer TNF alpha activity, e.g. to treat autoimmune diseases and cancer TNF alpha activity e.g. to treat autoimmune diseases and cancer TNF alpha antibody (Ab) heavy chain complementarity C factor alpha (TNF alpha) antibody (Ab) heavy chain complementarity C factor alpha (TNF alpha) antibody (Ab) heavy chain complementarity C determining region 3 (CDR3).

The present sequence is a novel anti-human tumour necrosis factor alpha (TNF alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Koff rate constant of 1x10 power -3 m or less that the constant of 1x10 power -1 or less (both determined by surface plasmon resonance), and cless (both determined by surface plasmon resonance) and cless (both determined by surface plasmon resonance).

C cardiac or inflammatory bone disorders, bone resorption distances, clearons the detricts of control disturbances.
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10-FEB-1997; U02219.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC;
                                                                                                                                                                                                     alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease;
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                                                                                                    endothelial
                                                                                                                                                   pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
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                                                                                                                           leukocyte adhesion
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Pred. No. 7.15e-01;
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C determining region 3 (CDR3).

C The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or 1 less and has a Koff rate constant of 1x10 power -3 s power -1 or 1 less (both determined by surface plasmon resonance), and 1 cell less (both determined by surface plasmon resonance), and 2 cell less (both determined by surface plasmon resonance), and 2 cell less (both determined by surface plasmon resonance), and 2 cell less (both determined by surface plasmon resonance), and 3 cell less (both determined by surface plasmon resonance), and 2 cell less (both determined by surface plasmon to 1x10 power -7 M or less. The Ab, which 2 cell less (both determined by surface plasmon to 1x10 power -7 M or less. The Ab, which 2 cell less (both disconsisting the continuous disconsisting the surface plasmon disconsisting the surface power cell less (both disconsisting the plasmon cell less (burns, reperfusion injury, kalold formation, scar tissue formation
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                                                                                                                                                                                                                                                                                                                                                                                                            leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 73; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salfeld JG, Schoen WPI; 97-415302/38
                                                                        W27587 standard; peptide; 12 AA. W27587;
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-1997; U02219.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                           Anti-TNF-alpha
                                                      19-MAR-1998
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a antibody heavy chain CDR3.
necrosis factor-alpha; TNF-alpha; antibody; CDR3:
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J. 3.52e+00;
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factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy multiple

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC syndrome, inflammatory bone disorders, bone resorption disease,

CC syndrome, inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC andothelial cells (HUVEC) (CIAM-1) on human umbilical vein
                                                                                                                                19-MAR-1998 (first entry)
Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; bunn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 73; 102pp; English.
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25-NOV-1996; US-031476.
09-FEB-1996; US-599226
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W27593 standard; peptide; 12
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Cocal Similarity 100.0%;
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No. 3.52e+00;
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14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BADI ) BASF AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
C=1f=1d JG. Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                Mankovich JA, McGuiness B
Salfeld JG, Schoenhaut D,
WPI; 97-415302/38.
                                                                      (BADI ) BASF AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Mankovich JA, McGuiness BT, Vaughan TJ, White M, Wilton
                                                                                                                                                                                                keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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W27594;
19-MAR-1998 (first entry)
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09-FEB-1996; US-599226.
       The present sequence is a novel anti-hufactor-alpha (TNF-alpha) antibody (Ab)
                               TNF alpha activity, e.g. to treat au Disclosure; Page 75; 102pp; English.
                                                                                                               09-FEB-1996; US-
(BADI ) BASF AG.
                                                       High affinity antibodies against human TNF
                                                                                                                                                                           WO9729131-A1.
                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 27;
Pred. No. 7.70e+00;
2; Mismatches 0
                     anti-human tumour necrosis
                                          autoimmune diseases and
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        heavy
                                                       alpha –
        chain
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        complementarity
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Best Local S
Matches
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THIGH affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and TNF alpha activity, e.g. to treat autoimmune diseases and Sclaim 9; Page 65; 102pp; English.

Claim 9; Page 65; 102pp; English.

C The present sequence is a novel anti-human tumour necrosic factor-alpha (TNF-alpha) antibody (Ab) heavy chain complete determining region 3 (CDR3).

C The Ab dissociates from TNF-alpha with a Kd of 1x10 power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s power less and has a Koff rate constant of 1x10 power - 3s 
                         less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an ICSO of 1x10 power -7 M or less. The Ab. whice inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gotty arthritis, altergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; factious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
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09-FEB-1996;
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14-AUG-1997.
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human umbilical vein endothelial cell.
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W27563;
19-MAR-1998 (fi:
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US-599226.
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1. No. 7.70e+00;
1. No. 7.70e+00;
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                                                   PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; DR WFI; 97-41530/238.

DR WFI; 97-41530/238.

PT High affinity antibodies against human TNF alpha - useful to inhibit PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer PS Claim 20; Page 74; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Koff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro CC inhibits TNF-alpha activity, can be used to treat sepsis, CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy multiple CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC sucrosis, periodontal disease, obesity and radiation disturbances, CC burns, reperfusion injury, kelold formation, scar tissue formation, CC andothelial cells (MTNF-alpha induced expression of endothelial cell cendothelial cells (MTNF-alpha induced expression of endothelial cell cendothelial cells (MTNF-alpha induced expression of endothelial cell
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Best Local
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

heavy chain; complementarity determining region 3; inhibition;

treatment; sepsis; disease; autoimmune disease; infectious disease;

malignancy; pulmonary disorder; intestinal disorder; hepatitis;

cardiac disorder; inflammatory bone disorder; reperfusion injury;

bone resorption disease; coagulation disturbance; burn; EHAM-1;

keloid formation; scar tissue formation; pyrexia; HUVEC;

periodontal disease; obesity; radiation toxicity;

endothelial cell leukocyte adhesion molecule-1;

human umbilical vein endothelial cell.
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endothelial cells
Sequence 12 AA;
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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W09729131-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W27592 standard; peptide; 12 AA.
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                                (HUVEC).
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90.0%;
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Pred. No. 1.67e+01;
1; Mismatches 0
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Query Match Best Local & Matches

Similarity

82.6%;

Score 57; DB 27; Pred. No. 1.67e+01 2; Mismatches

Length 12;

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                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and reutralises human TNF-alpha cytotoxicity in a standard in vitro 1293 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, vital or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukovyte adhesion molecule-1 (FIAM-1) on human umbilical wein
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Best Local
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W09729131-A1.
14-AUG-1997.
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Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Human; tumour necrosis factor-alpha; TNF-alpha; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; heaptitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
cardiac disorder; coaquiation disturbance; burn; ELAM-1;
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High affinity antibodies against human TNF alpha - useful to TNF alpha activity, e.g. to treat autoimmune diseases and collin 20; Page 74; 102pp; English.
The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complements.
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
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25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
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                        Anti-TNF-alpha antibody heavy chain variable region. Human; tumour necrosis factor-alpha; TNF-alpha; antibody; heavy chain; variable region; inhibition;
                                                                                                                            W27569;
19-MAR-1998 (first entry)
                                                                                                                                                                                 r 10
W27569 standard; Protein; 121 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukocyte adhesion
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Local Similarity 100.0%;
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   sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells (HUVEC).
12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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autoimmune disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 27;
Pred. No. 1.67e+01;
0; Mismatches 0
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i cancer
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NR WPI; 97-415302/38.

OR N-PSDB; T88404

PT High affinity antibodies against human TNF alpha - useful to inhibit PT High affinity antibodies against human TNF alpha - useful to inhibit PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer PS Claim 16; Page 76; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain variable region. CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Koff rate constant of 1x10 power -3 spower -1 or CC less (both determined by surface plasmon resonance), and CC neutralises human TNF-alpha cytotoxicity in a standard in vitro CC L929 assay with an TC50 of 1x10 power -7 M or less. The Ab, which CC inhibits TNF-alpha activity, can be used to treat sepsis, antoimmune diseases, e.g. rheumatoid arthritis, rheumatoid arthritis.
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14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
14-AUG-1997.
10-FEB-1997;
25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                         Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNP-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W27590 standard; peptide; W27590; 19-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease,
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Allen DJ,
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(BADI ) BASF AG.
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human umbilical vein endothelial cell.
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                              bone resorption disease; coagulation disturbance; keloid formation; scar tissue formation; pyrexia;
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                                                                                                                                                                                      human umbilical vein endothelial cell.
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JA, McGuiness BT, Roberts AJ, Sakorafas P,
Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AA;
                                                                                                                                                                                                                       disease; obesity; radiation toxicity;
cell leukocyte adhesion molecule-1;
US-031476.
US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUVEC).
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 AA
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Pred. No. 1.67e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 121;
                                                                                                                                                                                                                                                                                     HUVEC
                                                                                                                                                                                                                                                                                                                     ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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PREFERENCE STREET TO THE FERENCE STREET TO T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The present sequence is a novel anti-human tumour necrosis CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Knoff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro CC less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro CC less (both determined by surface plasmon resonance), and cc constant of 1x10 power -7 M or less. The Ab, which CC less (both determined by surface plasmon resonance), and vitro CC less (both section activity, can be used to treat sepsis, ca utoimmune diseases, e.g. rhematoid arthritis, rhematoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC clarosis, autoimmon diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC claros, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The CC pyrexia, periodontal disease, obesity and radiation toxicity. The condthelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canine IgE heavy chain constant region (exon 1-4 product). IgE; immunoglobulin; antibody; heavy chain constant region; altergy; hypersensitivity; therapy; dog; antisense; immunomodulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High affinity antibodies against human TNF alpha activity, e.g. to treat autoi Claim 20; Page 74; 102pp; English.
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Allen
                       21-AUG-1997.
14-FEB-1997; U02322.
14-FEB-1996; US-601197.
(IDEX-) IDEXX LAB INC.
                                                                                                                                                                      Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                       Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W23067;
19-FEB-1998
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  Harris
                                                                                                                          WO9730156-A2.
                                                                                                                                                                                                                         Misc_difference
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WPI; 97-415302/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mankovich JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asylstsfsld 11
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JA, McGuiness BT, Roberts AJ, Sakorafas P,
J, Schoenhaut D, Vaughan TJ, White M, Wilto
  Mermer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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174
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204
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90.98;
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Pred. No. 2.78e+01;
0; Mismatches 1
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AE;
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autoimmune diseases and
                                                                                                                                                                                                  TCC"
                                                                                                                                                    GAC"
                                                                                                                                                                                                                                                TGN"
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Best Local S
Matches
                                                                                                                                                                                                                                 Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated canine IgE heavy chain constant region DNA - useful to develop products for treatment of canine allergies and for immunomodulation in dogs

S Disclosure: Page 35-39; 59pp; English.

IgE heavy chain constant region (epsilon) genomic DNA. Another polypeptide; comprising the exon 5 and 6 product, is given in polypeptide, comprising the exon 5 and 6 product, is given in w23068. Recombinant peptides encoded by exons 1-6 can be produced in eukaryotic or prokaryotic cells. Such peptides, and antibodies raised against them, are used in methods to treat the manifestation of allergy in dogs, e.g. to treatment Type I immediate hypersensitivity, and for immunomodulation.
                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T07310
Mapping ligand binding d
expressing peptide(s) en
for ligand binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage US5464745-A.
            M. tuberculosis ORF 2 product.

MACE; mycolic acid cyclopropanating enzyme; cyclopropanation; pathogenic form; mycobacterium; non-pathogenic; screen; inhib; cyclopropane mycolic acid synthase; beta-ketoacyl reductase; Streptomyces cinnamonesis; homology.
                                                                                                                                                                                                                                                                                            can be so
Sequence
                                                                                                                                                                                                                                                                                                     Disclosure; Column 15-18; 12pp; English.

The phage T7 gene 10 leader sequence product (R87027) is encoded by prokaryctic expression vector pTOPE-1b(+) (T07310). A fusion of the leader sequence and a putative ligand-binding domain (LBD), esp. antigenic region, of a protein is obtd. following insertion of putative LBD-encoding DNA into the vector. The fusion protein accumulates as inclusion bodies in Escherichia coli host cells and can be screened for its ability to bind a ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1993; 040753.
31-MAR-1993; US-040753.
(NOVA-) NOVAGEN INC.
Garber R, Hammer B, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T7 gene 10 leader sequence product.
Plasmid pTOPE-1b(+); vector; ligand
                                                                                                     W06968
                                                                                                                   W06968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen;
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T7 gene 10 l
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Mycobacterium tuberculosis
                                                                                      2-MAR-1997
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)B; T79278.
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                                                                                                                   standard; Protein; 384
                                                                                                                                                                                                                                   Similarity 50.0% 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                            314 AA;
                                                                  (first entry)
sis ORF 2 product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Pred.
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Pred. No. 9.68e+01;
3; Mismatches 1
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                                                                                                                                                                                                                                 e 49; DB 15; Le
. No. 1.24e+02;
Mismatches 2;
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random gene fragments and testing
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                                                                                                                                                                                                                                                            Length 314;
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                                           inhibitor;
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PN W09829550-A1.

24-DEC-1998.

24-DEC-1996; ES-002770.

(INMU-) INMUNOLOGIA & GENETICA APLICADA SA.

(INMU-) INMUNOLOGIA & GENETICA APLICADA SA.

PI Casal Alvarez JI, Rodriguez Garcia MJ, Sanz Fernandez A;

PI Casal Alvarez JI, Rodriguez Garcia MJ, Sanz Fernandez A;

PI Casal Alvarez JI, Rodriguez Garcia MJ, Sanz Fernandez A;

PI WP; 98-388131/33.

PT New fusion proteins comprising Porcine Reproductive and Respiratory

Syndrome Virus nucleocapsid - useful as as reagents in immuno:diagnosis

PT New fusion protein seproducative in bacterial hosts

CC Inlis Sequence represents a fusion protein comprising the nucleocapsid

CC PRRSY) American isolate Canada 14/96 fused to the gene 10 protein from

CC Concerpsid (W68457) coding sequence into the bacterial expressed

CC uncleocapsid (W68457) coding sequence into the bacterial expressed

CC uncleocapsid (W68457) coding sequence into the bacterial expressed

CC uncleocapsid (W68457) coding sequence into the bacterial expressed

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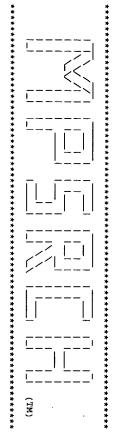
CC uncleocapsid (W68457) coding sequence into the bacterial expressed

CC uncleocapsid (W68457) coding sequence into the bacterial expressed
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PS Disclosure; Column 35-38; 35pp; English.
CC This sequence is encoded by ORF 2 of Mycobacterium tuberculosis (see
CC T46163). Three ORFs have been found all within a 7.2 kb BamHI fragment
CC isolated from M. tuberculosis, and are believed to be related to the
CC biosynthesis of mycolic acids. The ORF 2 gene product has homology to
CC known enzymes involved in the oxidative/reductive interconversions of
CC a ketone and an alcohol. It is most homologous (30 percent identity
CC over 188 amino acids) to actIII, beta-ketoacyl reductase from
Streptomyces cinnamonesis which is involved in chain elongation in
polyketide biosynthesis. Cycloproponation of mycolic acids distinguishes
pathogenic forms of mycobacterium from non-pathogenic forms. A method to
determine the ability of a cpd. to inhibit cycloproponation of mycolic
acids in pathogenic mycobacterium is claimed.
SQ Sequence 384 AA;
                                                                                                      Query Match
Best Local
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Best Local Similarity
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PRRSV isolate 14/96 nucleocapsid/phage T7 gene 10 fusion protein.
Nucleocapsid; Porcine Reproductive and Respiratory Syndrome Virus; PRRSV;
p1g; serum; RT-PCR; reverse transcription; amplification; fusion protein;
primer; bacteriophage T7; gene 10; E coli; immunoassay; diagnosis.
Chimeric - Porcine reproductive and respiratory syndrome virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 15
W68459 standard; protein; 386 AA.
                                                                                                                                                                              Sequence
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01-JUN-1995; US-457245.
(USGO) US GOVERNMENT.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                y Match 71.0%;
Local Similarity 50.0%;
71 aaylapgenldd 82
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54.5%;
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                                                                        Score 49; DB 36; Le
Pred. No. 1.24e+02;
4; Mismatches 2;
                                                                                                                         Length 386;
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                                                                        Indels
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Qy 1 ASYLSTSSSLDD 12
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Search completed: Thu Sep 2 12:35:05 1999 Job time: 20 secs.





Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Sep 2 12:37:02 1999; MasPar time 1.38 Seconds 88.598 Million cell updates/sec

abular output not generated.

Description: Perfect Score: Title: >US-08-599-226\_30 (1-12) from US08599226.pep 69 1 ASYLSTSSSLDD 12

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 15.800; Variance 47.088; scale 0.336

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
۳.	50	. 2	426	ω	PCT-US95-1	Sequence 2, Applicatio	- 1
2	50	72.5	426	<b>_</b>	08-3	equence 2, Applicat	3.45e+
ω	49	۳	$\vdash$	_	ò	equence 2, Applicat	4.46
4	49	1.	8	ب	US-08-457-	, Appli	4.4
υ	47		$\mathbf{r}$	2	us-08-761-	e 10, Applic	7.38
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7	47	68.1	213	ν	US-08-761-	5	7.3
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13	46		20	N	US-08-468-	ν,	9.47e+
14	46		21	2	US-08-787-	Ψ	9.4
15	46		7	N	US-08-327-	1,	9.47
16	45	ū	σ	4	5194425-4	o. 51944	. 21
17	45	5	ω	N	US-08-705-	Sequence 18, Applicati	1.21
18	44	63.8	209	ν	US-08-771-	Sequence 2, Applicatio	1.5
19	44	ω.	σ	_	US-07-688-	Sequence 16, Applicati	. 1.55e+02
20	44	ω.	σ	ω	PCT-US91-0	16,	<u>ب</u>
21	43	۲.	7	4	5194425-3	Patent No. 5194425.	. 98
22	43		7	N	US-08-227-	•	1.98e+
23	43		ω	N	US-08-928-	5, Applica	1.9

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
41	41	41	41	41	42	42	42	42	42	42	42	43	43	43	43	43	43	43	43	43	43
59.4	59.4	59.4	59.4	59.4	60.9	60.9	60.9	60.9	60.9	60.9	60.9	62.3	62.3	62.3	62.3	62.3	62.3	62.3	62.3	62.3	62.3
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3.21e+02	3.21e+02	3.21e+02	3.21e+02	3.21e+02			2.53e+02	2.53e+02	2.53e+02	2.53e+02	2.53e+02	1.98e+02									

## ALIGNMENTS

¥8×5 RESULT

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PCT-US95-13795-2

STANDARD;

PRT;

426 AA.

888888888888888888888888888	# <b>##</b> ##88888888888888888888888888888888
COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UNBER: PCT/US95/13795 FILING DATE: CLASSIFICATION: APPLICATION UNBER: PCT/US95/13795 FILING DATE: CLASSIFICATION: APPLICATION UNBER: PCT/US95/13795 FILING DATE: CLASSIFICATION: NAME: CARTY, CHRISTINE E. REGISTRATION NUMBER: 36,099 REFERENCE/DOCKET NUMBER: 19211Y TELECHMUNICATION INFORMATION: TELEPHONE: (908) 594-6734 TELEFAX: (908) 594-4720 INFORMATION FOR SED ID NO: 2: SEQUENCE CHARACTERISTICS: LEBROSTES SINGLE TOPDIORY: 10 noar MOLECULE TYPE: protein SEQUENCE 426 AA; 47234 MW; 1032622 CN;	Sequence 2, Application PC/TUS9513795  Sequence 2, Application PC/TUS9513795  GENERAL INFORMATION: GREGORY F. APPLICANT: HOLLIS, GREGORY F. APPLICANT: PATEL, MAYUR D. TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS NUMBER OF SEQUENCES: 4  CORRESPONDENCE ADDRESS: ADDRESSE: CHRISTINE E. CARTY STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000  CITY: RAHWAY STATE: NEW JERSEY COUNTRY: USA ZIP: 07065-0807

Sequence 2,

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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 426 maino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 426 AA; 47234 MW; 1032622 CN;
                           XXXXXX
                                               US-08-040-753-2
                                                                                                                                                           SEQUENCE
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                                                                                                     214 TSYLSPPSPLD 224
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FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 1921
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                       1 ASYLSTSSSLD 11
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APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                  ASYLSTSSSLD 11
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CITY: RAHWAY
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                                                                                                                               72.5%;
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                                               STANDARD;
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ER: 19211
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Pred. No. 3.45e+01;
3; Mismatches 1
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Pred. No. 3.45e+01
3; Mismatches
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Best Local Similarity 50.0%;
                                      GENERAL INFORMATION:
APPLICANT: BARRY III, Clifton E.
APPLICANT: YUAN, YING
TITLE OF INVENTION: CLONING AND EX
TITLE OF INVENTION: IN THE BIOSYNT
TITLE OF INVENTION: MYCOBACTERIUM
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                          XXXXXX
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                                                                                                                                                                                                                                                                          Sequence 5, Application US/08457245
                                                                                                                                                                                                        Sequence 5, Application US/08457245 Patent No. 5573915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION UNMBER: 27386
REFERENCE/DOCKET NUMBER: 70-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-9166
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAPPLICANT: NAPPLIC
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APPLICATION NUMBER: US/08/040,753
FILING DATE: 19930331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
JENCE 314 AA; 33533 MW; 495848 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: AMINO ACID
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CORRESPONDENCE ADDRESS:
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                       CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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STATE: WI
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1 South Pinckney St.,
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No. 5464745y, Robert
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Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                CLONING AND EXPRESSION OF DNA INVOLVED IN THE BIOSYNTHESIS OF CYCLOPROPANATED MYCOLIC ACIDS MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein Ligand Binding
Region Mapping System
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Pred. No. 4.46e+01;
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Best Local Similarity
Matches 6; Conse
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                                                                                                                                                                                                                                                                                                                                                                                            XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-761-258-10
                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08761258
                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08761258 Patent No. 5756087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 SSYLPTKAALD 245
                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Ligon, James M.

APPLICANT: Hill, Dwight S.

APPLICANT: Lam, Stephen T.

APPLICANT: Caffney, Thomas D.

APPLICANT: Torkewitz, Nancy

TITLE OF INVENTION: Genetically Modified Pseudomonas Strains

TITLE OF INVENTION: with Enhanced Biocontrol Activity

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Guy W.
REGISTRATION NUMBER: 30,617
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASYLSTSSSLD 11
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: ORF2 protein
ENCE 384 AA; 41963 MW; 701271 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                        STREET: 520 Which CITY: Tarrytown STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 384 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
           APPLICATION NUMBER:
                                                                                                 ZIP:
                                                                                                           COUNTRY:
                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                 10591
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: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                              E: Ciba-Geigy Corporation 520 White Plains Road, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steuart Street Tower, One Market Plaza
                                                                                                            USA
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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          US/08/761,258
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Pred. No. 4.46e+01;
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                                                                                                                                                Box 2005
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Best Local Similarity
Matches 4; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08287442
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08287442 Patent No. 5670350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: am....
TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYPE: 23392 MW; 2
                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/087,636

FILING DATE: 01-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/908,284

FILING DATE: 02-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/570,184

FILING DATE: 08-AUG-1990

ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 AGYLTKGAGINE 110
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (919) 541-8689 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASYLSTSSSLDD
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION UMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                           APPLICANT: Stein, Jeffrey I.
APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TITLE OF INVENTION: Gene Activating
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acid
                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                             COUNTRY: UZIP: 10532
                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                             CITY: Hawthorne
                                                                                                                                                                                                                                                                        ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
NAME: Elmer, James : REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i: 213 amino acids amino acid
                                                                                                                                                                                                                                                  New York
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Hill, Dwight S.
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Query Match
Best Local Similarity
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                                MOLECULE TYPE: SEQUENCE 213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein SEQUENCE 213 AA; 23364 MW; 236956 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 AGYLTKGAGLNE 110
                                                                               TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
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                                         TYPE: amino acids
TOPOLOGY: 1:----
VOLECITY

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                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION UNMER: 38,241
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genetically MCTITLE OF INVENTION: with Enhanced NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                      STREET: 520 Whit CITY: Tarrytown STATE: NY COUNTRY: USA
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TOPOLOGY:
                                                                                                                                                                               FILING DATE:
                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                      APPLICATION NUMBER:
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Hill, Dwight S.
Lam, Stephen T.
Gaffney, Thomas D.
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                               protein
23364 MW;
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                                                                                                                                                                                                                                        Floppy disk
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                                                                                                                                                                                                                                                                                                                                                        Genetically Modified Pseudomonas Strains
                                                                                                                                                                                      US/08/761,258
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7; M
 Score 47; DB 2; L
Pred. No. 7.38e+01;
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                                236956 CN;
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                                                                                                                                                                                                                                                                                                                                              Biocontrol Activity
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          Length 213;
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Query Match 68.1%;
Best Local Similarity 33.3%;
Matches 4; Conservative
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                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                     TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                APPLICATION UNMBER: US 07,
FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 08-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ASYLSTSSSLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                      NAME: Elmer, James Scott REGISTRATION NUMBER: 36,129 REFERENCE/DOCKET NUMBER: CGGTELECOMMUNICATION INFORMATION: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TITLE OF INVENTION: Gene Activating Element
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 01-JUL-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 02-JUN-19
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                   MOLECULE TYPE:
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                                                            TYPE: ami
TOPOLOGY:
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                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CIBA CL. ADDRESSEE: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                        LE TYPE: protein
213 AA; 23364 MW; 236956 CN;
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                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                 213 amino acids
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Hill, Dwight S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stein, Jeffrey I
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                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CIBA-GEIGY Corporation
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                                                                                                                                                                                                                  UMBER: US 07/908,284
02-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                              US 07/570,18
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 Pred.
           Score 47; DB 1; L
Pred. No. 7.38e+01;
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  Mismatches
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                   Length 213;
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  Indels
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 Gaps
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  Query Match
Best Local Similarity
Matches 4; Consei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08459174 Patent No. 5710031
                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/
FILING DATE: 08-AUG-1994
APPLICATION NUMBER: US 08/
FILING DATE: 01-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                   TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:||: :::|::
1 ASYLSTSSSLDD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stein, Jeffrey I.
APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TITLE OF INVENTION: Gene Activating Element
NUMBER OF SEQUENCES: 9
                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8614
                                                                                                                                                                                    FILING DATE: 08-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/908,284
FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/570,184
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                                               MOLECULE TYPE:
ENCE 213 AA;
                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                 REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08 FILING DATE: 02-JUN-1995
                                                                                             LENGTH:
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New York
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amino acid
GY: linear
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Hill, Dwight S.
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             68.1%;
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23364 MW;
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NUMBER: US 08/087,636
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Score 47; DB 1; L
Pred. No. 7.38e+01;
7; Mismatches 1
                                               236956 CN;
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                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/287,442
FILING DATE: 08-AUG-1994
APPLICATION NUMBER: US 08/087,636
FILING DATE: 01-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,284
FILING DATE: 02-JUL-1992
                                                                                                         TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICATION NUMBER: US 07,
FILING DATE: 08-AUG-1990
ATTORNEY_AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,12
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APPLICANT: Howell, Charles R.
APPLICANT: Becker, J. Ole
TITLE OF INVENTION: Gene Activating Element
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                           MOLECULE TYPE: protein JENCE 213 AA; 23364 MW; 236956 CN;
                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Boli-
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COUNTRY:
                                                                TOPOLOGY:
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            68.1%;
33.3%;
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 Score 47; DB 1;
Pred. No. 7.38e+01
7; Mismatches
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MOLECULE TYPE: protein
SEQUENCE 213 AA; 23364 MW; 236956 CN;
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 Sequence
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                                                                                                                                                                                                                                                             TELEFAX: (919) 541-8689 INFORMATION FOR SEQ ID NO:
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APPLICANT: Torkewitz, Nancy
TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
TITLE OF INVENTION: with Enhanced Biocontrol Activity
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION UMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELECHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O.
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
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                    Application PC/TUS9306300A
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 Application PC/TUS9306300A
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Hill, Dwight S.
Lam, Stephen T.
Gaffney, Thomas D.
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Pred. No. 7.38e+01;
7; Mismatches 1; Indels
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99 AGYLTKGAGLNE
                                   / Match 68.1%;
Local Similarity 33.3%;
                                               TYPE: and linear TOPOLOGY: linear MOLECULE TYPE: protein MOLECULE 213 AA; 23364 MW; 2:
                                                                                                                              TELEFAX: (919)541-868: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/0630
FILING DATE: 02-JUL-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                      FILING DATE: 02-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 02-JUL-1992
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                       REFERENCE/DOCKET NUMBER: S-18210/A/CGC1506/PC
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120 Marquette D
Cary, NC 27513
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Brvan, TX 77802
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3725 Surry Trail
Hillsborough, NC
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311 Melanie Lane
Cary, NC 27511
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Riverside, CA 92506
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Raleigh, NC 27613
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                            Score 47; DB 3; L
Pred. No. 7.38e+01;
7; Mismatches 1
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                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
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Local Similarity 45.5%;
hes 5; Conservative
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                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
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APPLICANT: Miller, Ariel
APPLICANT: Al-Sabbagh, Ahmad
APPLICANT: Al-Sabbagh, Ahmad
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
NUMBER OF SEQUENCES: 25
                                                                                                                                                           MOLECULE TYPE: NO. 5858980e
JENCE 20 AA; 2160 MW; 2047 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
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TOPOLOGY: lir
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OPERATING SYSTEM:
SOFTWARE: FastSE
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Pred. No. 9.47e+01;
5; Mismatches 1
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TELEX: 200154
TELEX: 200154
TELEX: POR SEQ ID NO: 3?
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 21 amino acids
                                                                                                                                                                        XXXXXX
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                   Sequence 1, Application US/08327357A
                                                                                                                                                                                               US-08-327-357A-1
                                                                Sequence 1, Application US/08327357A Patent No. 5817629 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Local Similarity 45.5%;
nes 5; Conservativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: WARREN, K
APPLICANT: CATZ, Ing
APPLICANT: CATZ, ITTLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                  1 ASYLSTSSSLD 11
                                                                                                                                                                                                                                                                          6 SKYLATASTMD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 081
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
JENCE 21 AA; 2312 MW; 2012 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & ADDRESSEE: Fish & Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08787547
                                     WARREN, Kenneth G. CATZ, Ingrid
                                                                                                                                                                                               STANDARD;
 PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND THE ADMINISTRATION OF MYELIN PEPTIDES TO MUTIPLE SCLEROSIS PATIENTS
                                                                                                                                                                                                                                                                                                                 Score 46; DB 2; I
Pred. No. 9.47e+01;
                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08191/003001
                                                                                                                                                                                               170
                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                             Length 21;
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              BASIC
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PROTEIN

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88888888888888888888
Search completed: Thu Sep Job time: 9 secs.
                                                                                                      Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/327,357A
FILING DATE: 21-OCT-1994
CLASSIFICATION NUMBER: US 07/798,099
FILING DATE: 27-NOV-1991
PRIOR APPLICATION NUMBER: US 07/798,099
FILING DATE: 27-NOV-1991
PRIOR APPLICATION NUMBER: CA 2,053,799-0
FILING DATE: 22-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Thnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 27052-115469
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
IMMEDIATE SOURCE:
CLONE: human myelin basic protein
SEQUENCE 170 AA; 18459 MW; 143992 CN;
                                                                     12 SKYLATASTMD 22
: ||:|:|:|
                                                    : ||:|:|::|
1 ASYLSTSSSLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Venable
STREET: 1201 New 'STREET: Mashington
STATE: D.C.
COUNTRY: USA
            2 12:37:11 1999
                                                                                                       Score 46; DB 2; Ler
Pred. No. 9.47e+01;
5; Mismatches 1;
                                                                                                                                  Length 170;
                                                                                                          Indels
                                                                                                        0;
                                                                                                        Gaps
                                                                                                        0
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\*\*\*\*\*\* (MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Sep 2 12:35:24 1999; MasPar time 3.47 Seconds 138.694 Million cell updates/sec

ibular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-599-226-30 (1-12) from US08599226.pep 69 1 ASYLSTSSSLDD 12

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 23.804; Variance 27.163; scale 0.876

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Sult No.	Score	% Query Match	Length	DB	ID	ptio	z
_	55	79.7	377	2	F71520	hypothetical protein	3.98e-01
2	51	٠	471	N	w	_	.11e+
ω	50	72.5	293	N	D70108	77	5.12e+00
4	49		345	۳	VABPA7	major capsid protein	8.36e+00
ហ	49		381	N	G71906	ble tran	8.36e+00
თ	49	71.0	398	ب	VBBPA7	minor capsid protein	
7	49	71.0	437	N	JC5459		8.36e+00
œ	49	•	650	N	F70974	probable acrAl protei	8.36e+00
9	48	•	239	N	S25204	srmX protein - Strept	1.35e+01
10	48	•	396	N	C49904	L-lactate dehydrogena	1.35e+01
11	48	•	483	N	A55033	kerătin 12 - mouse	1.35e+01
12	48	•	687	2	A41905	ferric vibriobactin r	1.35e+01
μ ω	48	69.6	750	2	S55180	phospholipase D homol	1.35e+01
14	47	68.1	213	N	A38222	regulatory protein ga	•
15	47	68.1	333	N	S42424	al protei	2.18e+01
16	47	•	471	N	S08325	flavonol 3-0-glucosyl	2.18e+01
17	47	68.1	471	N	S01052	flavonol 3-0-glucosyl	•
18	47	68.1	471	N	S01037	flavonol 3-0-glucosyl	2.18e+01
19	47	68.1	578	N	S26577	beta-hemolysin - Aero	2.18e+01
20	47	68.1	684	N	G70744	hypothetical protein	2.18e+01
21	47	68.1	792	N	C71250	probable cation-trans	•
22	46	66.7	115	N	D32055	nifW protein - Azotob	3.47e+01
23	46	66.7	128	ب	MBRTS	myelin basic protein	3.47e+01

45	44	43	42	41	40	39	38	37	3 6	<u>3</u> 5	34	ω G	32	31	30	29	28	27	26	25	24
45	45	45	45	45	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46
					66.7						•	•	66.7		66.7	66.7	66.7	66.7	66.7	•	66.7
1298	561	543	416	147	3924	1091	832	564	467	433	433	411	381	347	328	301	236	197	171	167	132
N	N	N	N	N	N	N	N	N	N	N	ᆫ	N	N	Ь	_	N	Ŋ	<u>_</u>	_	N	N
A64157	A31994	S56830	H64984	A69198	S37431	A58532	S71788	S57124	S10364	S04665	VBBPA3	S45318	G64607	VABPA3	MBMSB	S13095	S60941	MBHUB	MBCZB	A37246	H70759
hypothetical protein	keratin 10, type I, e	probable purine nucle		hypothetical protein	ankyrin 2, neuronal l	glial cell membrane g	P/CAF protein - human	CTP synthase (EC 6.3.	Ω		minor capsid protein	keratin 12 - rabbit (		major capsid protein	golli-myelin basic pr	P34 protein - Rickett	probable membrane pro	basic	basic	myelin basic protein	hypothetical protein
5.49e+01	5.49e+01	5.49e+01	5.49e+0	5.49e+01		3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01	3.47e+01

## ALIGNMENTS

RESULT 2  ENTRY  hypothetical protein - Arabidopsis thaliana ORGANISM  cress  #variety  03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change ACCESSIONS  REFERENCE  #authors  Dean, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveren, M.;	Query Match 79.7%; Score 55; DB 2; Length 377; Best Local Similarity 66.7%; Pred. No. 3.98e-01; Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps Db 324 ASYLSSSPSVED 335      : : :   Qy 1 ASYLSTSSSLDD 12	#cross-references MUID:9900809 #accession F71520 ##status #molecule_type DNA ##residues 1-377 ##label ARN ##cross-references GB:AE001312; GB:AE001273; NID:g3328812; PID:g3328818 ##cross-references MID:900809 ##cross-references GB:AE001312; GB:AE001273; NID:g3328812; PID:g3328818 ##cross-references GB:AE001312; GB:AE001273; NID:g3328818	ACLESSIONS A71570 A71570 REFERENCE A71570 **Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, R.L.; Zhao, Q.; Koonin, E.V.; Davis, R.W.  #journal Science (1998) 282:754-759 #title humans: Chlamwdia trachomatis	D. strain UW3/Cx)  D. strain UW3/Cx)  #formal_name Chlamydia trachomatis 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_c 21-Nov-1998
nge	aps 0;	g3328818	Marathe,	hange

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Stiekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel,
K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.;
Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.;
Gielen, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.;
Lecharny, A.; Auborg, S.; Gy, I.; Kreis, M.; Lao, N.;
Kavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger,
Kavanagh, T.; Hempel, S.; Kotter, A.; Pulgdomenech, P.; Douka,
M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.;
James, R.; Montfort, A.; Pons, A.; Pulgdomenech, P.; Douka,
A.; Voukelatou, E.; Milloni, D.; Hatzopoulos, P.;
Piravanndi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.;
Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.;
Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny,
M.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klosterman, S.;
#journal Nature (1998) 391:485-488
Analysis of 1.9 Mb of contiguous sequence from chromosome 4
#cross-references MUID:98121113
#cross-references MUID:98121113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSIONS
REFERENCE
     Best Loc
Matches
                                                     Query Match
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                                                                                                                                                                                                                                                                                                                            #cross-references MUI
#accession D70108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #map_position 4COP9-4G3845
MARY #length 471 #molecular-weight 52785 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-471 ##label
##cross-references GB:Z97342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
                                                                                                                                                            ##cross-references GB:AE001120; GB:AE000783; NID:g2687951; PID:g2687956; TIGR:BB0068
                                                                                                                                      ##experimental_source strain B31
                                                                                                                                                                                                                       ##residues
                                                                                                                                                                                                                                           ##molecule_type DNA
                                                                                                                                                                                                                                                                                                        ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
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Local Similarity 63.6%;
les 7; Conservative
        Local Similarity
nes 6; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _
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                                                                                                                                                                                                                                                                                                                                                                                                  Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hikkey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Yugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C. Nature (1997) 390:580-886 Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #formal_name Borrelia burgdorferi #common_name Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein BB0068 - Lyme disease
  72.5%;
larity 60.0%;
Conservative
                                                                                                             #length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-Jun-1998
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                                                                                                                                                                                                                                                                                                                                                                                    burgdorferi
                                                                                                                                                                                                                                                                                                                                                        MUID: 98065943
                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown;
translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary; nucleic acid sequence not
translation not shown
                                                                                                                                                                                                                    1-293 ##label KLE
                                                                                                             293 #molecular-weight 33278 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #sequence_revision 13-Feb-1998 #text_change
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Pred. No.
3; Misma
Score 50; DB 2; Ler
Pred. No. 5.12e+00;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BEV
NID:g2245031; PID:e327038; PID:g2245065
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                                                        Length 293;
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RESULT ENTRY

ş 밁 SUMMARY GENETICS

Matches Best

DATE

ORGANISM TITLE

SUMMARY

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#map_position ECLASSIFICATION #KEYWORDS
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#note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSIONS
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Best Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                            #authors Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.; G.F.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #variety
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                                       ##molecule_type DNA
##residner
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##cross-references EMBL:V01146; NID
##note the authors did not
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##residues 1-381 ##label ARN
##cross-references GB:AE001496; GI
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57.51-60.49
#superfamily phage T7 major capsid protein
capsid protein
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J. Mol. Biol. (1983) 166:477-535

Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genetic elements.
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#formal_name phage T7
#fort Escherichia coli
13-Jun-1983 #sequence_revision 30-Sep-1990 #text_change
26-Feb-1999
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12-Feb-1999
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GB:AE001439; NID:g4155191; PID:g4155196
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Best Local Similarity 50.0%;
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#cross-references MUID:83241725
#accession $42326
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                                                                                                                                                                                                                                                                                  71 AAYLAPGENLDD 82
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Local Similarity 45.5%;
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                                                                                                                                     JC5459 #type complete inulin fructotransferase (depolymerizing) (EC 2.4.1.93) precursor - Arthrobacter sp. Inulase II; Inulin fructotransferase (DFA-III-producing)
                                                                                                                                                                                                                                                                                                                                                                                                translation of the nucleotide sequence involves frameshift within codon 341 superfamily phage T7 major capsid protein 10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                10B
57.51-60.49
Sakurai, H.; Yokota, A.; Tomita, F.
Biosci. Biotechnol. Biochem. (1997) 61:87-92
Molecular cloning of an inulin fructotransferase
(depolymerizing) gene from Arthrobacter sp. H65-7
expression in Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       minor capsid protein 10B - #formal_name phage T7 host Escherichia coli
                                                                                                                 #formal_name Arthrobacter sp.
17-Jun-1997 #sequence_revision
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Pred. No. 8.36e+00;
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Pred. No. 8
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166:477-535
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Best Local Similarity 54.5%;
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Best Local Similarity 50.0%;
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33-437
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#title
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#accession JC5459
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                                                                                                                                                                                                                                                 ##residues 1-650 ##label COL
##cross-references GB:AL009198; GB:AL123456;
##CTOSS-references GB:AL009198; GB:AL123456;
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This enzyme is thermotolerant and metal ions resistant protein. It is also stable for the industrial preparation of di-D-fructofuranose 1,2':2,3' dianhydride. It converts inulin into di-D-fructofuranose 1,2':2,3' dianhydride through
                                          501 SSYLPTKAALD 511
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##cross-references DDBJ:D84399; NID:g1906791; PID:d1019710; PID:g1906792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
Nature (1998) 393:537-544
Deciphering the biology of Mycobacterium tuberculosis from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intramolecular transfructosylation.
                                                                                                                                                                         #length 650
                                                                                                                                                                                                                                                                                                                                                                                              F70974
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17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable acrAl protein - Mycobacterium tuberculosis (strain
H37RV)
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    #status predicted #label MAT
pth 437 #molecular-weight 46475 #checksum 9304
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                                                                                                                                                                       #molecular-weight 70939
                                                                                                        Score 49; I
Pred. No. 8.
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Pred. No. 8.36e+00;
                                                                                        Mismatches
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                                                                                                        DB 2; I
8.36e+00;
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                                                                                                                          Length 650;
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                                                               ##experimental_source strain K-12,
REFERENCE S47666
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #title Three overlapping lct genes involved in by Escherichia coli. #cross-references MUID:94012541
   #submission
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                                 #authors
                                                                                                                                                                                                                                                                                     #title The complete genome sequence of Escherichia coli K-12
#cross-references MUID:97426617
#accession G65160
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                                                                                                                 ##Status ##molecule_type DNA ##nolecule_type D
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##mollecule_type DNA
##residues 1-396 ##label DON
##cross-references GB:L13970; NID:g404692; PID:g404695
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Similarity 45.5%;
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srmx protein - Streptomyces ambofaciens

#formal_name Streptomyces ambofaciens

28-May-1993 #sequence_revision 28-May-1993 #text_change
Plunkett, G. submitted to
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$25202
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Escherichia coli
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#length 239
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11-Nov-1994 #sequence_revision
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es EMBL:X63451; NID:g46699;
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EMBL Data Library, March 1994
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No. 1.35e+01;
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Best Local Similarity 33.3%;
Matches 4; Conservative
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Best Local Similarity 50.0%;
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#title
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                                                                                    #authors
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#residues 1-118,'X',120-396 ##label PLU
##cross-references EMBL:U00039; NID:g466582;
                                                                                                                                                                                                                                                                                                                         131 ASYLGKVRSLEE 142
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##cross-references GB:U08095; NID:9565659; PID:9565660
##note authors translated the codon ATC for re
and GCG for residue 388 as Arg
FICATION #superfamily cytoskeletal keratin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu, C.Y.; Zhu, G.; Converse, R.; Kao, C.W.C.; Tseng, S.C.G.; Mul, M.M.; Seyer, J.; Justice M.E.; Hansen, G.M.; Kao, W.W.Y. J. Biol. Chem. (1994) 269:24627-24636 Characterization and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FMN;
               J. Bacteriol. (1992) 174:3729-3738
Cloning, sequencing, and transcriptional regulation of viua,
the gene encoding the ferric vibriobactin receptor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain (S)-2-hydroxy-acid oxidase homology #label
#active_site His #status predicted
#length 396  #molecular-weight 42728  #checksum 9705
                                                                                                                                                   ferric vibriobactin receptor ViuA - Vibrio cholerae
iron-siderophore complex receptor ViuA
#formal_name Vibrio cholerae
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_ch
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keratin 12 - mouse
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                                                                                  Butterton, J.R.;
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18-Nov-1994 #sequence_revision 18-Nov-1994 #text_cl
17-Mar-1999
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Pred. No. 1.35e+01;
3; Mismatches 3
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Pred. No. 1.35e+01;
7; Mismatches 1
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                                                                                    J.A.;
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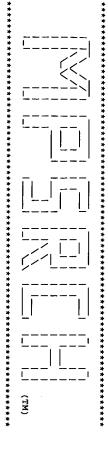
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#map_position
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues ##ross-references GB:U11759; GB:M90461; NID:g517206; PID:g531822
##cross-reference extracted from NCBI backbone (NCBIN:104700)
##note NCBIP:104701)
                                                                                                                                                                                       ##molecule_type DNA
##molecule_type DNA
##label KAF
###TOO:Idnes 1-750 ##label KAF
                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-750 ##label KAW ##residues 1-750 ##label KAW ##cross-references EMBL:249407; NID:gl008335; PID:gl008336; MIPS:YJL132w
                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
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##cross-references EMBL:X87371; NID:g854542;
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                                354 YLAVSAPLED 363
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Local Similarity 60.0%;
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 YLSTSSSLDD 12
                                                                                Similarity
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#length 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome X reveals 14 known genes and 13 new open reading frames including homologues of genes clustered on the right arm of chromosome XI.
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protein J0678
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Yeast (1996) 12:787-797
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$55159
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phospholipase D homolog YJL132w - yeast
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08_Jul-1995_#sequence_revision 01-Sep-1995 #text_change
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                                                                Conservative
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50.0%;
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Pred. No. 1.35e+01;
4; Mismatches 0
                                                                                Score 48; I
Pred. No. 1
                                                                  Mismatches
                                                                                                                                                                               NID:g854542; PID:g854564
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                                                                                DB 2;
1.35e+01
                                                                                               Length 750;
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                                                                             Query Match 68.1%;
Best Local Similarity 41.7%;
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##residues 1-333 ##label CIR
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Local Similarity 33.3%;
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#length 333
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                                                                                                                                                                                                                                                                                  Cirillo, J.D.; Weisbrod, T.R.; Pascopella, L.; Bloom, B. Jacobs Jr., W.R. W.R. Mol. Microbiol. (1994) 11:629-639
Isolation and characterization of the aspartokinase and aspartate semialdehyde dehydrogenase operon from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G: Haas, D.
G: Haas, D.
G: Haas, D.
Proc. Natl. Acad. Sci. U.S.A. (1992) 89:1562-1566

Global control in Pseudomonas fluorescens mediating
Global control in Pseudomonas fluorescens mediating
Global control in Pseudomonas fluorescens mediating
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#formal_name Pseudomonas fluorescens
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
05-Dec-1997
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NCBIP:85373)
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#binding_site phosphate (Asp) (covalent) #statu
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                                                              Score 47; DB 2;
Pred. No. 2.18e+01
6; Mismatches
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Pred. No. 2.18e+01
7; Mismatches
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Search completed: Thu Sep 2 12:35:41 1999 Job time: 17 secs.



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:36:23 1999; MasPar time 4.43 Seconds
147.813 Million cell updates/sec

Title: >US-08-599-226-30 Description: (1-12) from US08599226.pep Perfect Score: 69
Sequence: 1 ASYLSTSSSLDD 12

Searched: 179066 seqs, 54579741 residues

Scoring table:

PAM 150 Gap 15

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: Mean 23.424; Variance 25.983; scale 0.902

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		do .			SUMMARIES		
esult No.	Score	Query Match	Length	₽B	ID	Description	Pred. No.
1	55	79.7	377	2	084397	HYPOTHETICAL 41.4 KD P	3.17e-01
N	53		127	14	011696	AGME	9.36e-01
ω	51	73.9	471	10	023552		
4	50	72.5	293	N	051095	CONSERVED HYPOTHETICAL	
ъ	49	71.0	188	10	081650	THYMIDYLATE KINASE (FR	
σ	49	71.0	384	ν	Q11197	HYPOTHETICAL 41.9 KD P	7.51e+00
7	49	71.0	437	N	008305	INULIN FRUCTOTRANSFERA	7.51e+00
8	49		650	N	050417	MULTI-FUNCTIONAL ENZYM	7.51e+00
ø	49		1022	σ	Q28628	A-KINASE ANCHORING PRO	7.51e+00
10	48	69.6	160	5	Q27302	GLOBIN.	1.24e+01
11	48		239	N	200510	SRMX PROTEIN.	1.24e+01
12	48		484	ű	Q23173	W05E10.1 PROTEIN.	1.24e+01
13	48		649	w	060167	PROTEIN COMPLEX ASSEMB	1.24e+01
14	48		1758	5	Q22830	SIMILAR TO HUMAN SREBP	
15	47	68.1	112	N	068946	DINITROGENASE 3 DELTA	2.03e+01
16	47	68.1	213	N	069157	RESPONSE REGULATOR.	2.03e+01
17	47	68.1	471	Ų	061986	DYSTROPHIN-LIKE PROTEI	
18	47	68.1	696	υ	Q23264	ZC373.1 PROTEIN (FRAGM	2.03e+01
19	47	68.1	792	N	083999	CATION-TRANSPORTING AT	
20	47	68.1	931	10	004026	HYPOTHETICAL 104.6 KD	2.03e+01

44	4.	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
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55 55	65.2	5	5	65.2	Ġ	66.7	σ	66.7	σ	$\boldsymbol{\sigma}$	O	66.7	66.7	σ	g	66.7	g	66.7	$\mathbf{a}$	66.7	S.	66.7	68.1
853 10 1043 !	852 10	583 5	473 (			2697 5		1128	1091 11			831 5											1548 5
0 Q42150 5 001757	_	-	4 Q16402		2 068943			1 051999		_		5 Q21574						0122				1 061836	5 001583
BETA-GALACTOSIDASE LIK SIMILAR TO ACHLYA AMBI	BETA-GALACTOSIDASE.	10.	TYPE I KERATIN 16.		DINITROGENASE 3 DELTA	SIMILARITY TO THE P13/	REPJ PROTEIN.	REPI PROTEIN.	MEMBRANE GLYCOPROTEIN.	SRK29 PROTEIN KINASE.	P/CAF.	M28.8 PROTEIN.	RESPONSE REGULATOR.	GOLLI-MBP.	COSMID F28B12.	MYELIN BASIC PROTEIN (	COSMID ZK470.	CHROMOSOME XV READING	GOLLI-MBP.	MYELIN BASIC PROTEIN (	GLOBIN.	MYELIN BASIC PROTEIN (	SIMILAR TO SERINE/THRE
5.33e+01 5.33e+01					5.33e+01	3.31e+01	3.31e+01		3.31e+01		3.31e+01			3.31e+01	3.31e+01			3.31e+01		3.31e+01	3.31e+01	3.31e+0	2.03e+01

# ALIGNMENTS

RESU ID AC AC DT	Db Ma	RP RA	RERERE	RESU ID AC AC DT DT DT DT DT OS
Ol1696 PRELIMINARY; PRT; 127 J O11696; O1-JUL-1997 (TREMBLREL. 04, CREATED) 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE	Query Match  Query Match  Best Local Similarity 66.7%; Pred. No. 3.17e-01;  Matches 8; Conservative 4; Mismatches 0  Db 324 ASYLSSSPSVED 335      : : :   Qy 1 ASYLSTSSSLDD 12	RP SEQUENCE FROM N.A.  RP SEQUENCE FROM N.A.  RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J.,  RA MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO  RA DAVIS R.W.;  RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA  DR EMBL; AE001312; G3328818;  KW HYPOTHETICAL PROTEIN.  SQ SEQUENCE 377 AA; 41449 MW; 2B79B006 CRC32;		SUL
AA. UPDATE)	; Length 377; -01; 0; Indels 0; Gaps 0;	J., MARATHE R., ARAVIND L., AO Q., KOONIN E.V., ATA BANKS.	J., MARATHE R., ARAVIND L., AO Q., KOONIN E.V., ar Pathogen of Humans:	PDATE) UPDATE) MYDIA.

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NUCLEOPROTEIN (FRAGMENT).
MEASLES VIRUS (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
     BORRELIA BURGDORFERI (LYM
BACTERIA; SPIROCHAETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; 297342; E327038;
HYPOTHETICAL PROTEIN.
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J. MED. VIROL. 52:113-120(1997).
EMBL: D8/487; D10/20995; -.
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PROTEIN.
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     E DISEASE SPIROCHETE).
SPIROCHAETACEAE; BORF
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
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ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     293
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2.69e+00;
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9.36e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC32
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                                                                                                                                                                                                                          UPDATE)
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.D 081650 Ph...
D 081650;
AC 081655;
AC 081655;
DT 01-NOV-1998 (TREMBLREL 06, LAS1 01-NOV-1998 (TREMBLREL 08, LAS1 01-NOV-1998 (TREMBLREL 08, LAST ANNOL...
DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOL...
DE THYMIDYLATE KINASE (FRAGMENT).
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
CUKARYOTA; VIRIDIPLANTAE; STEEPTOPHYTA; EMBRYOPHYT EUPHYLLOPHYTES; SPERMATOPHYTA; MACNOLIOPHYTA; EUC ""RALES; BRASSICACEAE; ARABIDOPSIS."

FITES R.C.;

FITES R.C.;

FITES R.C.;
  RESULT

ACCORDANCE

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Best Local S
Matches
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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

C STRAIN-ATCC 35210 / B31;

C MEDLINE; 98055943.

X MEDLINE; 98055943.

X FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.

A LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., (A.)

A DOUGHERTY B., TOMB J.-F., FLEISCHWANN R.D., RICHARDSON D.,

PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANG.

A PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANG.

A VUGT R., PALMER N., ADAMS M.D., GOCANNE J.D., WEIDMAN J.,

AU UTTERBACK T., WATTHEX L., MCDONALD L., ARTIACH P., BOWMAN C.,

A GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATC

GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATC

"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Consei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

ULLAH H., ROBERTSON N., FITES R.C.;

"Plant thymidylate kinase mRNA.";

SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF081570; G3493131; -.

NON_TER 1
1
SEQUENCE 188 AA; 21248 MW; C306E7B8 CRC32;
                                                                                                                                             MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA;
ACTINOMYCETALES; CORYNEBACTERINEAE; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATURE 390:580-586(1997).
EMBL; AE001120; G2687956;
TIGR; BB0068; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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58.3%;
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       G.S., BELISLE e involved in t
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
N IN CMA1 3'REGION (ORF2
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred.
4; M
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Pred. No. 7.51e+00
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                                                                                                                                               A; ACTINOBACTERIDAE; MYCOBACTERIACEAE; M
       the
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4.51e+00;
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PHYTA; EUDICOTYLEDONS;
       .T., BARRY C.E
e biosynthesis
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of;
                                                                                                                                                  MYCOBACTERIUM
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Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                       ULT 8
050417; PRELIMINARY;
050417; OT-JUN-1998 (TREMBLREL. 0
01-JUN-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  008305;
01-JUL-1997
01-JUL-1997
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE: 97179800.

SAKURAI H., YOKOTA A., TOMITA F.;

"Molecular cloning of an Inulin fructotransferase
"Molecular cloning of an H65-7 and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEH

FAMILY (SDR),

EMBL; U27357; G886103; -.

PFAM; PF00106; adh_short; 1.

HYPOTHETICAL PROTEIN; OXIDOREDUCTASE.

SEQUENCE 384 AA; 41995 MW; 9FF8465A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   008305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyclopropanated mycolic acids in Mycobacterium tuberculosis."; PROC. NATL. ACAD. SCI. U.S.A. 92:6630-6634(1995).
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDU
                                                                                                                                          MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA;
ACTINOMYCETALES; CORYNEBACTERINEAE; M
                                                                                                                                                                                                                                                                                                                                                                                                     BIOSCI. BIOTECHNOL. BIOCHEM. 61:87-92(1997).
EMBL; D84399; D1019710; -.
TRANSFERASE; GLYCOSYLITANSFERASE.
SEQUENCE 437 AA; 46475 MW; DC74B68C CRC32;
                     PARKHILL J., BARRELL SUBMITTED (NOV-1997)
                                            SEQUENCE FROM N.A.
STRAIN-H37RV;
                                                                                OLIVER K., SKELTON J. SUBMITTED (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIA; FIRMICI ACTINOMYCETALES;
SEQUENCE FROM N.A.
                                                                                                          STRAIN-H37RV;
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                            MULTI-FUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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(TREMBLREL.)
                                                                                                                                                                                                                                                       PRELIMINARY;
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54.5%;
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                                                                                BADCOCK K., CHURCHER C.M., HA
D EMBL/GENBANK/DDBJ DATA BANKS
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04, LAST SEQUENCE UPDATE)
09, LAST ANNOTATION UPDATE)
E (EC 2.4.1.93).
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06,
06,
                      EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                     Score 49;
Pred. No.
6; Misma
                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; I
Pred. No. 7.
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                            A; ACTINOBACTERIDAE;
MYCOBACTERIACEAE; MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                 DB 2; L
. 7.51e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437
                                                                                                                                                                                                                                                        650
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7.51e+00;
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                      DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                           Length 437;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (depolymerizing)
on in Escherichia
                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 9
ID Q28628;
AC Q28628;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANOTATION UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANOTATION UPDATE)
DT 01-KINASE ANCHORING PROTEIN AKAP120.
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC CHKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUT
CE EUKARYOTA; METAZOA; CHORDATA; TORTEBRATA; MAMMALIA; EUT
CE EUKARYOTA; METAZOA; CHORDATA; TORTEBRATA; MAMMALIA; EUT
CE EUKARYOTA; METAZOA; TISSUE-STOMACH;
RY SEQUENCE FROM N.A.
RY SEQUENCE FROM N.A.
RY TIGENELID D.T., YEH J.L., BRADFORD A.J., GOLDENRING J.
RANSFIELD D.T., YEH J.L., BRADFORD A.J., GOLDENRING J.
RY TIGENELIFICACION and Characterization of a novel A-kinas
RY TIGENELIFICACION (AKAP120) from rabbit gastric parietal cells.";
BIOCHEM. J. 322:0-0(0).
EMBL; UZ6360; G3399584; -.
SQ SEQUENCE 1022 AA; 116903 MW; 98BD43C2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
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                                                                           SORRE PROCESS OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local
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Query Match
                                                                                                      KLOEK A.P., GOLDBERG D.E.;
SUBMITTED (FEB-1996) TO EMBL/GEN
EMBL; 048291; G1203913; -.
EMBL; 048290; G1203913; JOINED.
EMBL; 048289; G1203909; -.
PFAM; PF00042; globin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SIRAIN=NEW ZEALAND WHITE; TISSUE-STOMACH;
STRAIN=, PROVIDED TO THE STORY OF THE STOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROC.
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PHILIPP W.J., POULET S., EIGLMEIER K.,
BALASUBRAMANIAN V., HEYM B., BERGH S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        CAENORHABDITIS BRIGGSAE.
EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "An integrated map of the genome of the tubercle Mycobacterium tuberculosis {\tt H37Rv}, and comparison
                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     RHABDITINA; RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLOBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLE S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       935 AYLSTISSLKD 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 SSYLPTKAALD 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYLSTSSSLDD
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AL009198; E120
ENCE 650 AA;
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Similarity 54.5%;
6; Conservative
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                                                                           160
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llarity 72.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                           AA;
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E1202309; -.
AA; 70939 MW;
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                                                                    18591 MW;
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   . 68
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10,
10,
                                                                                                                                                                                                                                                                                                                                                                                                  DDA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
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1; Mismatc
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Pred. No.
4; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93:3132-3137(1996)
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                                                                       618F4F46 CRC32;
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7.51e+00;
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7.51e+00;
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BLOOM B.R., JF
   DВ
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ن.
                                                                                                                                                                                                                                                         DATA BANKS
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Length 160;
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RESULT
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Best Local
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Matches
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01-NOV-1996
01-JAN-1999
W05E10.1 PRO
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01-NOV-1996
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Q00510;
                                                                                       WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONHAMMER E., STALER R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VANGHAN K., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a polyketide synthase gene in Strepto.
MOL. MICROBIOL. 6:2019-2029(1992).
EMBL; X63451; G46702; -
SEQUENCE 239 AA; 26493 MW: 458PCE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q23173
Q23173;
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MEDLINE; 92374852.
GEISTLICH M., LOSICK R., TURN
"Characterization of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREPTOMYCES AMBOFACIENS.
BACTERIA; FIRMICUTES; ACTINOBACTER
ACTINOMYCETALES; STREPTOMYCINEAE;
                             NATURE 368:32-38(1994).
EMBL; 277670; E1350053;
                                                                            elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRMX PROTEIN
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                           MORTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHABDITINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W05E10.1
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                                                                                   "2.2 Mb of contiguous elegans.":
                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
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277670; E1550;
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5; Conservative
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5 (TREMBLREL.
9 (TREMBLREL.
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(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHABDITOIDEA;
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45.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEMATODA;
             53896
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09,
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GENBANK/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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LAST SEQUENT ANNUAL AST ANNUAL AST
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Pred. No. 1.24e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST ANNOTATION UPDATE)
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           EC00CF7B CRC32;
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Mismatches 1;
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RESULT 14

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Matches
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Best Local Similarity
Matches 5; Conser
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01-AUG-1998
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060167
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSON J., PERCY C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                            WU X., LE
SUBMITTED
                                                                                                                                                                                                                                                                                                                        "ATSON A., WELLIGATE TO THE TRANSPORT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BECK A., REINHARDT R., WOOD V
SUBMITTED (MAY-1998) TO EMBL/C
EMBL; AL023594; E1293401; -.
SEQUENCE 649 AA; 72985 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHIZOSACCHAROMYCES POMBE (FISSION EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHISCHIZOSACCHAROMYCETALES; SCHIZOSACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SIMILAR TO HUMAN SREBP-2 BASIC-HELIX-LOOP-HELIX-LEUCINE
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EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPBC19F8.03C
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    SEQUENCE FROM N.A WATERSTON R.;
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 NYLSTARSLE :|||: ||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 AYVAASSTLED
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                                                                                                                                 (DEC-1995)
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(TREMBLREL.
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07, LAST
                                                                                                                                 EMBL/GENBANK/DDBJ
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Pred. No. 1.24e+01;
6; Mismatches 0
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Pred. No. 1.
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O68946; PRELIMINARY; PRT; 112 AA.

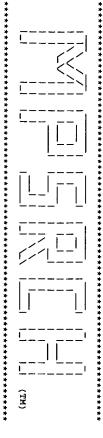
O68946; O1-AUG-1998 (TREMBLREL. O7, CREATED)

O1-AUG-1998 (TREMBLREL. O7, LAST SEQUENCE UPDATE)

O1-AUG-1998 (TREMBLREL. O7, LAST ANNOTATION UPDATE)

DINITROGENASE 3 DELTA SUBUNIT.
                                                                                                                                                                              SEQUENCE FROM N.A.
LOVELESS T.M., BISHOP P.E.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF058780; G3065908; -.
SEQUENCE 112 AA; 13273 MW; 5ABCB39C CRC32;
                                                                                                                                                                                                                                                              AZOMONAS MACROCYTOGENES.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; AZOTOBACTERACEAE;
AZOMONAS.
[1]
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1 ASYLSTSSSLDD 12
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                                                                                                                   Score 47; DB 2; Length 112;
Pred. No. 2.03e+01;
4; Mismatches 1; Indels
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:35:58 1999; MasPar time 2:17 Seconds 156.010 Million cell updates/sec

ibular output not generated.

Title: Description: Perfect Score: >US-08-599-226-30 (1-12) from US08599226.pep 69 1 ASYLSTSSSLDD 12

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 24.293; Variance 24.652; scale 0.985

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

esult No.	Score	Query Match	Length D	BB	ID	Description	Pred. No.
1	49	71.0	345	- :	VCAA_BPT7	MAJOR CAPSID PROTEIN 1	3.05e+00
2	49	71.0	. 352	1	YDH3_SCHPO	HETICAL 39.7	3.05e+00
ω	49	۲.	398	_	VCAB_BPT7	PROTEIN	
4	48	9.	396	_	FLDD_ECOLI	L-LACTATE DEHYDROGENAS	5.18e+00
ر.	48	69.6	483	Н	K1CL_MOUSE	KERATIN, TYPE I CYTOSK	
σ	48	9	687	1	VIUA_VIBCH	VIBRIOBACTIN RECEPTOR	
7	48	9	750	_	YJN2_YEAST		5.18e+00
œ	47	68.1	213	1	GACA_PSEFL	JLATO	8.71e+00
9	47	68.1	333	1	YASD_MYCSM	HYPOTHETICAL 35.9 KD P	8.71e+00
10	47	68.1	471	1	UFO1_MAIZE	FLAVONOL 3-0-GLUCOSYLT	8.71e+00
11	47	68.1	471	1	UFO3_MAIZE	FLAVONOL 3:0-GLUCOSYLT	
12	47	68.1	471	۲	UFO2_MAIZE	FLAVONOL 3-O-GLUCOSYLT	8.71e+00
13	47	68.1	578	1	HLY4_AERSA	HEMOLYSIN 4 PRECURSOR.	8.71e+00
14	47	68.1	684	_	YV18_MYCTU	HYPOTHETICAL 57.3 KD P	8.71e+00
15	46		115	1	NIFW_AZOVI	NIFW PROTEIN.	1.45e+01
16	46	66.7	127	1	MBP_RAT	MYELIN BASIC PROTEIN S	1.45e+01
17	46	66.7	132	_	YW07_MYCTU	14.7	1.45e+01
18	46	66.7	167	<b> </b> 4	MBP_CAVPO	MYELIN BASIC PROTEIN (	1.45e+01
19	46	66.7	171	۲	MBP_PANTR	MYELIN BASIC PROTEIN (	1.45e+01
20	46	66.7	194	۲	MBP_MOUSE	MYELIN BASIC PROTEIN (	1.45e+01
21	46	66.7	196	٢	MBP_HUMAN		1.45e+01
22	46	66.7	301	دبم	P34_RICRI		1.45e+01
23	46	66.7	347		VCAA_BPT3	MAJOR CAPSID PROTEIN 1	1.45e+01

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7 431 1 VALE_RABIT KERMILN, TIVE 1 CT 7 433 1 VAB_BPT3 MINOR CAPSID PROTE 7 466 1 FILD_SALTY FLAGELLAR HOOK-ASS 7 577 1 PYRH_YEAST CTP SYNTHASE 2 (ECC 7 1839 1 ANKC_HUMAN ANKYRIN, BRAIN VAR 7 3924 1 ANKB_HUMAN ANKYRIN, BRAIN VAR 132 1 ANFG_AZOVI NITROGENASE IRON-1 2 103 1 NAFG_AZOVI NITROGENASE IRON-1 2 104 1 VELL_ECOLI HYPOTHETICAL 43.4 2 416 1 KICL_HUMAN KERATIN, TYPE I CY 2 446 1 KICL_HUMAN KERATIN, TYPE I CY 2 456 1 KICL_HUMAN KERATIN, TYPE I CY 2 471 1 KICL_HUMAN KERATIN, TYPE I CY 2 471 1 KICL_HUMAN KERATIN, TYPE I CY 2 494 1 KICL_HUMAN KERATIN, TYPE I CY 2 526 1 KICL_BOVIN KERATIN, TYPE I CY 2 527 1 MERA_STAAU MERCURIC REDUCTASE 543 1 YJFB_YEAST HYPOTHETICAL 60.8 593 1 KICL_HUMAN KERATIN, TYPE I CY 547 1 MERA_STAAU MERCURIC REDUCTASE 547 1 MERA_STAAU MERCURIC REDUCTASE 548 1 XICL_HUMAN KERATIN, TYPE I CY 549 1 KICL_HUMAN KERATIN, TYPE I CY 540 1 MERCURIC REDUCTASE 547 1 MERA_STAAU HYPOTHETICAL 71.0 548 1 YJFB_YEAST HYPOTHETICAL PROTE
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# ALIGNMENTS

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RESULT 2 ID YDH3_SCHPO STANDARD; PRT; 352 AA. AC Q92348; DT 01-NOV-1997 (REL. 35, CREATED) DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)	COAT PROTEIN. SEQUENCE 34 Query Match Best Local Simil Matches 6; 71 AAYLAPGE	This SWISS-PROT entry is copyric between the Swiss Institute of the European Bioinformatics Institution use by non-profit institution modified and this statement is rentities requires a license agree or send an email to license edish EMBL; V01146; G15604;  PIR; A04344; VABPA7.  PIR; S42325; S42325.	BACTERIOPHAGE T7.  VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILE [1] [1] SEQUENCE FROM N.A. MEDLINE; 83241725. DUNN J.J., STUDLIER F.W.; "Complete nucleotide sequence of bacterioph locations of T7 genetic elements."; J. MOL. BIOL. 166:477-535(1983)!- SIMILARITY: TO THE T3 MAJOR CAPSID PROT	RESULT 1  VOAZA_BET7  STANDARD; PRT; 345 AA.  P19726; P03717;  T 21-JUL-1986 (REL. 01, CREATED)  DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)  DE MAJOR CAPSID PROTEIN 10A.  SN 10.

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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                   VCAB_BPT7 ; STANDARD; P19727; P03717; 21-JUL-1986 (REL. 01, CREATED) 01-FEB-1991 (REL. 17, LAST SEQ 01-FEB-1991 (REL. 17, LAST ANN
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                                                                 PIR;
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-I- THE MINOR CAPSID PROTEIN 10B
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                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  DUNN J.J., THOMPSON
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SCHIZOSACCHAROMYCETACEAE;
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DB 1; L
3.05e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFIA H.J., BURLAND V., DANIELS D.L., PLU;
"Analysis of the Escherichia coll genome.
"egion from 76.0 to 81.5 minutes.";
NUCLEIC ACIDS RES. 22:2576-2586(1994).
-!- CATALYTIC ACTIVITY: (S)-LACTATE + 2 FI
2 FERROCYTOCHROME C.
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P33232;
                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                 ACT_SITE
                                                                                                                                                                                                                                                                                                      PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L13970;
EMBL; U00039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 94316500.
SOFIA H.J., BURLAND V.,
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STRAIN=K12 / MGI
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STRAIN-K12
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BACTERIA; PROTEOBACTERIA;
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                                                                                                                                                                                                          ACT_SITE
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01-FEB-1994 (REL. 28, LAST SEQUENCE UF
01-NOV-1997 (REL. 35, LAST ANNOTATION
1-LACTATE DEHYDROGENASE (CYTOCHROME) (
                                       208 SAYLGKPTGLED
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   ASYLSTSSSLDD
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TE: PS00557; FMN_HYDROXY_ACID_DH;
PF01070; FMN_dh; 1.
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TO THE FMN-DEPENDENT ALPHA-HYDROXY
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7; M
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REMOVES THE SUBSTRATE ALPHA-PROTON AS THE FIRST STEP IN CATALYSIS (BY SIMILARITY).

SUBSTRATE BINDING (BY SIMILARITY).

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1. No. 5.18e+00;
Mismatches 1;
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(EC 1.1.2.
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in L-lactate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLUNKETT G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FERRICYTOCHROME
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Best Local Similarity
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KRT12 OR KRT1-12 OR KRT1.12.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
EUKARYOTA; METAZOA; CHORDATA; WURIDAE; MURINAE; MUS.
                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                         VARSPLIC VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U02880; G414540; -. EMBL; U08095; G565660; -. MGD; MGI:96687; KRT1-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced th between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine keratin gene Krt1.12.";
J. BIOL. CHEM. 269:24627-24636(1994).
-i- FUNCTION: MAY PLAY A UNIQUE ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SVJ; TISSUE-CORNEA; MEDLINE; 95014223.
LIU C.-Y.. ZHU G., CONVERSE R., TSENG S.C.-G., MUI M.-M., SEYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
KERATIN, TYPE I CYTOSKELETAL 12 (CYTOKERATIN 12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATI
KERATIN 3 ASSOCIATES WITH KERATIN 12.
-!- TISSUE SPECIFICITY: CORNEA-SPECIFIC. ASSOCIATED MAINLY WITH
LAYERS OF THE CENTRAL CORNEAL EPITHELIUM AND ALSO FOUND IN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSENG S.C.-G., MUI M.-M., SEYER J., JUSTICE M.: HANSEN G.M., KAO W.W.-Y.; "Characterization and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIU C.-Y., ZHU G., WESTERHAUSEN-LARSON SUN T.-T., KAO W.W.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K1CL_MOUSE
Q64291;
                                                                     SEQUENCE
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00226; IF; 1. PFAM; PF00038; filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE SPLICING. -!- SIMILARITY: BELONGS T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUPRABASAL LIMBAL EPITHELIUM.
THERE ARE TWO TYPES OF CYTOSK
I (ACIDIC) AND II (NEUTRAL TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS: DIFFERENT FORMS MAY
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428
69.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                     MW;
                                                                                TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
COIL 2B.
COIL 22.
COIL 2.
COIL 2.
YE -> KL (IN K12-ALT9).
MISSING (IN K12-ALT9).
Score
Pred.
                                                                                                                                                                                                                                                                  ROD.
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                                                                  54DB7635 CRC32;
No.
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                                                                                                                                                                                                                                                                                                                                     HEPTAD REPEAT PATTERN;
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  DB 1; I
5.18e+00;
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                    Length 483;
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RESULATION OF THE PROPERTY OF 
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                                                                                                         P47014;

P47014;

O1-FEB-1996 (REL. 33, CREATED)

O1-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)

O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

HYPOTHETICAL 84.5 KD PROTEIN IN MRS3-URA2 INT.

YJL132W OR JO678.

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)

SACCHAROMYCES CEREVISIAE (BAKER'S HEMIASCOMYCETES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q00964;
01-APR-1993
01-APR-1993
15-DEC-1998
SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
MEDLINE; 96408771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, sequencing, and transcriptional regulation of viuA, the gene encoding the ferric vibriobactin receptor of Vibrio cholerae.";
J. BACTERIOL. 174:3729-3738(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIAO W.J., CHOI M.H., BUTTERTON J.R.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA
-!- FUNCTION: RECEPTOR FOR FERRIC VIBRIOBACTIN
                                                                                   EUKARYOTA; FUNGI; A SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                           YJN2_YEAST
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PFAM; PF00593; TonB_boxC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-OGAWA
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                                                                                                                                                                                                                                                                                                                                                                                  662 YLSTNNTLDQ 671
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Similarity 60.0%;
6; Conservative
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687 1
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                                                                                   ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCES.
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Pred. No. 5.
4; Mismatc
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5.18e+00;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                       synthesis and PROC. NATL. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CHA0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYANIDE CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
RESPONSE REGULATOR GACA (GLOBAL ACTIVATOR) (GLOBAL ANTIBIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X87371; G854564; -. EMBL; Z49407; G1008336; -
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YEAST 12:787-797(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KATSOULOU C., TZERWIA M., TAVERNARAKIS N., ALEXANDRAKI D.; "Sequence analysis of a 40.7 kb segment from the left arm of chromosome X reveals 14 known genes and 13 new open reading including homologues of genes clustered on the right arm of
                       <del>-</del>
                                                                                                                   Pseudomonas fluorescens biological control strain.";
MOL. PLANT MICROBE INTERACT. 7:455-463(1994)
-i- FUNCTION: INVOLVED IN THE REGULATION OF SECONDARY METABOLISM.
INVOLVED IN THE SYNTHESIS OF THE ANTIFUNGAL FACTORS CYANIDE A
                                                                                                                                                                                                                                                                                             MEDLINE; 94355677.
GAFFNEY T.D., LAM S.T.,
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                         TITH
                                                                                                                                                                                                                                                                                                                                                                                                                    "Global control in Pseudomonas fluorescens mediating antibiotic synthesis and suppression of black root rot of tobacco."; PROC. NATL. ACAD. SCI. U.S.A. 89:1562-1566(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAVILLE J.,
                                                                                                                                                                                            "Global regulation of expression of antifungal factors by seudomonas fluorescens biological control strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          932967;
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                    SIMILARITY:
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SIMILARITY: TO OTHER BACTERIAL REGULATORY PROTEINS INVOLVED
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MEDLINE; 94254720.
CIRILLO J.D., WEISE
JACOBS W.R. JR.;
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CONFLICT
SEQUENCE
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HYPOTHETICAL 35.9 KD PROTEIN IN ASD 3'REGION
MYCOBACTERIAM SMECHATIS.
BACTIROMYCETALES; CORYNEBACTERIAE, MYCOBACTE
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EMBL; L29642; G472403; -.
PROSITE; PS00622; HTH_LUXR_FAMILY;
                                                                                     EMBL; Z17372; G581353; -. HYPOTHETICAL PROTEIN. SEQUENCE 333 AA; 35881
                                                                                                                                                                                                                                                                                                                                                                        "Isolation and characterization of the aspartokinase and semialdehyde dehydrogenase operon from mycobacteria."; MOL. MICROBIOL. 11:629-639(1994).
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HSSP; P10957; 1RNL.
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GENETICS 119:185-197(1988).
-!- FUNCTION: IN THE PRESENCE OF OTHER
-!- FUNCTION REACTION ALLOWS THE A
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EMBL; X07940; G22205; -.
PIR; S01052; S01052.
PIR; S08324; S08324.
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01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 31, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 14, LAST SEQUENCE OF SEQUE
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FURTEK D., SCHIEFELBEIN J.W., JOHNSTON F., NELSON O.E.
"Sequence comparisons of 3 wild-type bronze-1 alleles
PLANT MOL. BIOL. 11:473-481(1988).
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA;
      FLAVONOL
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3-O-D-GLOCOSIDE.
3-O-D-GLOCOSIDE.
PATHWAY: ONE OF THE ESSENTIAL
PATHWAY: ONE OF THE ESSENTIAL
ANTHOCYANIN BIOSYNTHETIC PATHW
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                                                                                                                                                                                                                                                                                                                          SFLSTASSLAQ
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FERASE; GLYCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
990 (REL. 14, CREATED)
990 (REL. 14, LAST SEQUENCE UPDATE)
997 (REL. 35, LAST ANNOTATION UPDATE)
3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZEA.
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Pred. No. 8.71e+00;
3; Mismatches 1
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of mai
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      (UDP-GLUCOSE FLAVONOID
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SIDA; POALES;
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RESULTANGE OF THE PROPERTY OF 
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Best Local S
Matches
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P16165;
01-APR-1990
                                                                                                                                                                                                                                                                                                                       01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ELAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-NC2 ALLELE).
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genetic fine structure.";
GENETICS 119:185-197(1988).
-!- FUNCTION: IN THE PRESEN
"Sequence comparisons of 3 wild-t
PLANT MOL. BIOL. 11:473-481(1988)
-!- FUNCTION: IN THE PRESENCE OF
                                                                                                                                                                                                                ZEA MAYS (MAIZE).
EUKARYOTA; VIRIDIPLANTAE;
EUPHYLLOPHYTES; SPERMATOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00375; UDPGT; 1.
PFAM; PF00201; UDPGT; 2.
TRANSFERASE; GLYCOSYLTRANSFERASE.
SEQUENCE 471 AA; 48673 MW; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
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BZ1 OR UGT71A1.
ZEA MAYS (MAIZE).
                                                                                             FURTEK D.,
                                                                                                                          SEQUENCE
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                                                                                                                                                                                       POACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
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PATHWAY: ONE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC
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                                         FROM N.A.

SCHIEFELBEIN J.W., JOHNSTON

make the second se
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                                                                                                                                                                                                                    DIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRAC
SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA;
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63.6%;
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Pred. No. 8.71e+00;
3; Mismatches 1
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   OTHER NECESSARY COLOR
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                                                             NELSON O.E.
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                                                                                                                                                                                                                    TRACHEOPHYTA; SIDA; POALES;
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Best Local S
Matches
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Q08677;
01-NOV-1997 (REL. 3
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01-NOV-1997 (REL. 3
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 MICROB. PARTHOG. 15:269-282(1993).
-i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS
-i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS
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    SEQUENCE
                                               SIGNAL
                                                                                                   EMBL; x65049; G39012; - PFAM; PF00652; Ricin_B_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S08325; S08325.
MAIZEDB; 13885; -.
PROSITE; PS00375; UDPGT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
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                                                                          HEMOLYSIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and characterization of three hemolysin genes from Aeromonas salmonicida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94142497.
HIRONO I., AOKI T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASH4
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PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL STEPS IN THE ANTHOCYANIN BIOSYNTHETIC PATHWAY.

SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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FERASE; GLYCOSYLTRANSFERASE.
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    578
                                                                          TOXIN; SIGNAL.
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35, LAST SEQUENCE UPDATE)
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Pred. No. 8.71e+00;
3; Mismatches 1
                        POTENTIAL.
HEMOLYSIN 4
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    8A23C8BC CRC32;
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Q11157;
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01-APR-1990
01-APR-1990
15-JUL-1998
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PROSITE; PS00:
HYPOTHETICAL |
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 57.3 KD PROTEIN GMC-TYPE OXIDOREDUCTASE CY20G9.18C.
MTCY20G9.18C.
MTCY20G9.18C.
MYCOBACTERIUM TUBERCULOSIS.
BACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
-I- COFACTOR: FAD FLAVOPROTEIN (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z77162; E255032;
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                                                                                           SEQUENCE FROM N.A. MEDLINE; 89123097.
                                                                                                                                          AZOTOBACTER VINELANDII.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                NIFW
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                                                                                                                                 AZOTOBACTER.
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PS00624; GMC_OXRED_2; 1.
ICAL PROTEIN; OXIDOREDUCTASE; FLAVOPROTEIN;
684 AA; 72253 MW; F4A66D1F CRC32;
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larity 60.0%;
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36, LAST ANNOTATION
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70.0%;
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No. 8.71e+00;
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No. 8.71e+00;
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                                                                                                                                             AZOTOBACTERACEAE
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                                                          ERQUIST R.A.,
DEAN D.R.;
cluster from
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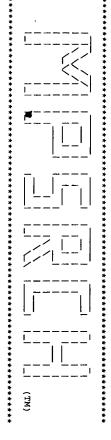
produced

through a collaboration

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Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       EMBL; M20568; G142365; -.
PIR; D32055; D32055.
NITROGEN FIXATION.
SEQUENCE 115 AA; 13418 MW; 74E9995C CRC32;
                                                       54 YLSKAGDLDE 63
||| :: ||:
3 YLSTSSSLDD 12
2 12:36:06 1999
                                                                                                                               Score 46; DB 1; Length 115;
Pred. No. 1.45e+01;
3; Mismatches 2; Indels
                                                                                                                                 0;
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                                                                                                                                 0;
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Séarch completed: Thu Sep Job time : 8 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 12:38:14 1999; MasPar time 3.62 Seconds 70.454 Million cell updates/sec

Title: >US-08-599-226-31
Description: (1-12) from US\u00fc8599226.pep
Perfect Score: 82
Sequence: 1 ASYLSTSFSLDY 12

Scoring table: PAM 150
Gap 15
Searched: 170751 segs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part33 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.911; Variance 64.247; scale 0.279

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Result
100 8 7 6 5 4 4 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO.
55334555555555555555555555555555555555	Score
100.0 81.7 78.0 74.4 74.4 67.1 67.1 67.1 67.1 67.1 67.1 67.1 67.1	Query Match
12 12 12 12 12 12 12 12 12 12 12 12 12 1	Length
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W27590 W27593 W27593 W27592 W27596 W27586 W27586 W27586 W27589 W27587 W27589 W27589 W27589 W27589 W27589 W27589	ID
Anti-TNF-alpha antibo	Description
2.71e-01 8.27e+00 1.61e+01 3.10e+01 3.10e+01 1.12e+02	Pred. No.

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# ALIGNMENTS

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neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple	less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and		The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity	TNF alpha activity, e.g. to treat autoimmune diseases and cancer Claim 20; Page 74; 102pp; English.	High affinity antibodies against human TNF alpha - useful to inhibit	aughan TJ, White M, Wi	Sakorafas P	(BADI ) BASK AG. Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,	09-FEB-1996; US-599226. CMV		10-FEB-1997; U02219.	WU9/29131-A1. 14-AUG-1997.	Homo sapiens.	human umbilical vein endothelial cell.	endothelial cell leukocyte adhesion molecule-1;	keloid formation; scar tissue formation; pyrexia; HUVEC;	bone resorption disease; coagulation disturbance; burn; ELAM-1;	cardiac disorder; inflammatory bone disorder; reperfusion injury;	malignancy: nulmonary disease; autoimmune disease; infectious disease;	heavy chain; complementarity determining region 3; inhibition;	antibody.	19-MAR-1998 (first entry)	W27590;	

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PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI High affinity antibodies against human TNF alpha - useful to inhibit

TNF alpha activity, e.g. to treat autoimmune diseases and cancer

CC Laim 20; Page 73; 102pp; English.

The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity

CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmo resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1299 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autioned diseases, e.g. rheumatoid arthritis, rheumatoid

CC scherosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC scherosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC scherosis, autoimmune diabetes, autoimmune resorpation disease,

CC burns, reperfusion injury, kelold formation, scar tissue formation,

CC curdiac, periodontal disease, obesity and radiation toxicity. The
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disease; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
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Sequence 1
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                                        pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
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25-NOV-1996; US-031476.
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Similarity 100.0%;
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12 AA;
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Pred. No. 2.71e-01;
0; Mismatches 0;
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Best Local Query

91 . 78;

Score Pred.

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DB 27; 8.27e+00;

Length 12

Anti-TNF-alpha antibody heavy chain CDR3. Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

Anti-TNF-alpha

19-MAR-1998 (first entry)

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The Ab dissociates from TNP-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNP-alpha cytotoxicity in a standard in vitro 1929 assay with an ICS0 of 1x10 power -7 M or less The Ab, which inhibits TNP-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiaco or inflammatory bone disorders, bone resorption disease, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
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Sequence 1
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WPI; 97-415302/38.

High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Heavy chain; complementarity determining region 3; inhibition;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                      W27591 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
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                           Homo sapiens.
WO9729131-A1.
14-AUG-1997.
                                                                                                                            Anti-TNF alpha antibody heavy chain CDR3.

Human; tumour necrosis factor alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The balso inhibits TNF-alpha induced expression of endothelial cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W27592 standard; peptide; 12 W27592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukocyte adhesion molecule-1 (ELAM-1)
endothelial cells (HUVEC).
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25-NOV-1996; US-031476
09-FEB-1996; US-599226
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W09729131-A1.
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10-FEB-1997; U02219
                                                                                                                human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                       l9-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 27; Le
Pred. No. 3.10e+01;
0; Mismatches 2;
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Or
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Best Local
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WPI; 97-415302/38.

High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 74; 102pp; English.

Claim 20; Page 74; 102pp; English.
High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 16; Page 76; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain variables.
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W27569;
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wil
                                                                                                                          Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton WPI; 97-415302/38.
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                Homo sapiens.
W09729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-TNF-alpha antibody heavy chain variable region. Human; tumour necrosis factor-alpha; TNF-alpha; antibody; heavy chain; variable region; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 74: 102pp; English.
The present sequence is a novel anti-human factor-alpha (TNF-alpha) antibody (Ab) heav determining region 3 (CDR3).
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09-FEB-1996; US-599226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 121 AA.
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75.08;
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Pred. No. 3.10e+01;
2; Mismatches 1
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                                                                                                                                                                                      Labkovsky B,
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        variable
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Best Local S
Matches
The present sequence is a novel anti-human tumour necrosis

(factor-alpha (TWP-alpha) antibody (Ab) heavy chain complementarity

(determining region 3 (CDR3).

The Ab dissociates from TWF-alpha with a Kd of 1x10 power -8 M or

(less and has a Koff rate constant of 1x10 power -3 s power -1 or

(less (both determined by surface plasmon resonance), and

(conclusives human TWF-alpha cytotoxicity in a standard in vitro

(constant session with an IC50 of 1x10 power -7 M or less. The Ab, which

(constant TWF-alpha activity, can be used to treat sepsis,

(autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

(spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

(sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

(syndrome, infectious diseases, malignancy, pulmonary, intestinal,

(corriace or inflammatory bone disorders, bone resorption diseases,

alcoholic, viral or fulminant hepatitis, coagulation disturbances,

burns, reperfusion injury, keloid formation, scar tissue formation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 72; 102pp; English
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Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Saifeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton WPI; 97-415302/38.
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Human; tumour necrosis factor alpha; TNF-alpha; inhibition;
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larity 81.8%;
Conservative
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Pred. No. 3.10e+01;
1; Mismatches 1;
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                                                                                                          The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
determining region 3 (CDR3).
The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
neutralises human TNF-alpha cytotoxicity in a standard in vitro
1299 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, kelold formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
Ab also inhibits TNF-alpha induced expression of endothelial cell
ieukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
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10-FEB-1997; U02219.
25-NOV-1996; US-0314/6.
09-FEB-1996; US-599226.
(BADI ) BASE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disfurbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; pendothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukocyte adhesion molecule-1 (ELAM-1)
endothelial_cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 73; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salfeld JG, Schoenhaut D, WPI; 97-415302/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W27589 standard; peptide; 12 AA
                                                                                                 endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            numan umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 asylstsssld 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASYLSTSFSLD 11
    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                    Similarity
                                                                             L cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody
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90.9%;
                      90
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Pred.
                    Score
Pred.
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; DB 27;
No. 1.12e+02;
                    55; DB 27;
No. 1.12e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on human umbilical vein
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                                      Length
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to inhibit cancer
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PI Mankovich JA, McGuiness BT, Roberts AJ, Sakoratas P, PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; BR WPI; 97-415302/38.

DR WPI; 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer PT Claim 20; Page 73; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or Cless and has a Koff rate constant of 1x10 power -3 s power -1 or CC less and has a Koff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmor resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro CC inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC ardiac or inflammatory bone disorders, bone resorption disease, CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC ardiac or inflammatory bone disorders, bone resorption disease, CC burns, reperfusion injury, keloid formation, scar tissue formation, CC pyrexia, periodontal disease, obesity and radiation toxicity. The Naleviche adhesion molecule-1 (ELAM-1) on human umbilical vein condition of endothelial cells (HVFC)
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; time alpha diction; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; perfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                   Human/murine IL-1 chimeric antibody CL.

Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1; light; L; chain; constant; region; variable; mouse; anti-human; graft; CDR; complementarity determining region; heavy; H; inflammatory disease; arteriosclerosis; detection; diffused intravascular coagulation; leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
W09729131-A1.
                                                                                                                                                09-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                              endothelial cells
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1998 (first entry)
Anti-TNF-alpha antibody heavy chain CDR3.
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W27587 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                            1 asylstsssld 11
                                                                                                                                                                                                                                                                           ASYLSTSFSLD
                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           l cells
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                         Protein; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                              67.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 27; L6
Pred. No. 1.12e+02;
0; Mismatches 1;
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Claim 1, Page 30-31; 58pp; Japanese.

CC The sequences given in R47205-08 represent the light and heavy chain, convariable and constant regions of a chimeric recombinant antibody and constant region is that of a human antibody and constant region is that of a human antibody and constant region is that of a human antibody and constant region is that of a human antibody and constant region is that of a human antibody and conservation of the variable region is from a mouse anti-human II-1 antibody, and a heavy (H) chain in which the constant region is that constant region is that constant region is a mouse-human graft containing the CDR regions of conservation of is a mouse-human graft containing the CDR regions of conservation of its a mouse-human graft containing the CDR regions of conservation human II-1 antibody. The chimeric antibody is used to consuce anti-human II-1 antibody. The chimeric antibody is used to consuce anti-human graft containing the cDR regions of conservation or leakemia. It can also be labeled and used for conservation or leakemia. It can also be labeled and used for
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Best Local
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08-JUL-1993; J00941.

16-JUL-1992; JP-189248.

(SAKA) OTSUKA PHARM CO LTD.

Hirai Y, Nishida T, Omoto Y

WPI; 94-048885,06.
adultination vivo sites in vivo Claim 2; Fig 13; 58pp; Japanese. Claim 2; Fig 13; 58pp; Japanese.
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03-FEB-1994.
08-JUL-1993; :
16-JUL-1992; :
                                                                                                                                                       Mouse/human chimeric antibody against human interleukin-1 - for treatment of diseases in which production of interleukin-1 is abnormal, and for diagnostic imaging of interleukin-1 product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; chimeric; recombinant; antibody; human; interleukin-1; I light; L; chain; constant; region; variable; mouse; anti-human; graft; CDR; complementarity determining region; heavy; H; inflammatory disease; arteriosclerosis; detection; diffused intravascular coagulation; leukemia.
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09-AUG-1994 (first entry)
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                                                                                                                                                                                                                                                                                                 N-PSDB; Q56069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9402627-A.
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Hirai Y, Nishida T, Omoto Y,
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Similarity 50.0%;
5; Conservative
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Pred. No. 1.12e+02;
5; Mismatches 0
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                           the light and heavy chain.
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                                                                                                                                                            production
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Matches
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Best Local :
                                                                                                                                                                                                                                                                                               This sequence represents the heavy chain mature peptide of a chimeric recombinant antibody against human interleukin-1 (II-1). The chimeric antibody has a light (L) chain in which the constant region is that of a human antibody and the variable region is from a mouse anti-human II-1 antibody and an eavy (H) chain in which the constant region is that of a human antibody and the variable region is from a mouse anti-human II-1 antibody, and a heavy (H) chain in which the constant region is that of a human antibody and the variable region is from a mouse anti-human II-1 antibody or is a mouse-human graft containing the CDR regions of mouse anti-human II-1 antibody. The chimeric antibody is used to treat diseases in which abnormal amounts of II-1 are produced, eg. inflammatory disease, arteriosclerosis, diffused intravascular coagulation or leukement II can also be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse/human chimeric antibody against human interleukin-1 - for treatment of diseases in which production of interleukin-1 is abnormal, and for diagnostic imaging of interleukin-1 production sites in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric human/mouse antibody H chain mature peptide. Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1; Probe; chain; constant; region; variable; mouse; anti-human; PCR; graft; CDR; complementarity determining region; heavy; H; detection; inflammatory disease; arteriosclerosis; polymerase chain reaction; if the constant of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hirai Y, Nishida WPI; 94-048885/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1993; J00941.
16-JUL-1992; JP-189248.
(SAKA ) OTSUKA PHARM CO LTD.
Hirai Y, Nishida T, Omoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diffused intravascular coagulation; leukemia; amplify. Chimeric - Homo sapiens.
Chimeric - Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 19; 58pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R47211 standard; Protein; 147 AA. R47211;
                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT Rat interleukin-1 beta converting enzyme related protease - used for proteasting Alzheimer's disease, amyotrophic lateral sclerosis, and treating Alzheimer's disease, amyotrophic lateral sclerosis, and protease related protease, overexpression of the related protease, overexpression of which converting enzyme (ICE) related protease, overexpression of which converting enzyme (ICE) related protease. The amino acid converting enzyme (ICE) related protease is present in the rate brain cDNA library. ICE related protease is present in the central nervous system and is enriched in central neurons concluding pyramidal neurons and granule neurons of the hippocampus cand cerebral cortex. An expression vector capable of producing the ICE related protease in a host cell is claimed. The protease can be used in a claimed method to identify compounds that inhibit apoptosis. Such inhibitors can be used to treat Alzheimer's can be used to treat Alzheimer's chisese, amyotrophic lateral sclerosis (ALS), head trauma or other cased against the protease may be used dor diagnosis of these conditions states, or in their treatment.
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Best Local
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15-JUL-1997;
22-JUL-1996;
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Misc_difference 152
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N1 B, Paul SM, Wu X;
WPI; 98-120767/11.
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                                               Misc_difference
                                                                                                                                                                                         Misc_difference
                                                                                                                                                                                                                                            Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                 Candida albicans oligopeptide transporter. Oligopeptide transporter; OPT1 gene; fungianticandidal.
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W64560;
07-DEC-1998 (fi
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W47089 standard;
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3 436
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/note-
515
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474
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469
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CT This is the Candida albicans oligopeptide transporter, OPT1. Its amino acid sequence was deduced from an isolated genomic clone (see V49601) obtained through heterologous expression in Saccharomyces cerevisiae di-/tripeptide transport mutant PBIX-9B. When CL transformed with a plasmid harboring OPT1, mutant PXIX-9B, which conditions used, was conferred with an oligopeptide transport occurrence of the radiolabeled tetrasport activity under the conditions used, was conferred with an oligopeptide transport occurrence of the radiolabeled tetrasport protein increase in the initial cuptake rate of the radiolabeled tetrasportide Lys-Leu-Gly-(3H)Leu. The deduced protein product contains 12 hydrophobic regions, suggestive of a membrane transport protein. The oligopeptide curansporter facilitates the uptake of normally non-permeable drugs, and is especially used to target antifungals, specifically anti-Candida drugs, which are conjugated, linked or attached to the peptide being transported. It can also be used to identify plant coligopeptides as herbicides or growth stimulants.
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Best Local
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                                                                                                                                                                                                         16-MAY-1995; U06119.
16-MAY-1994; US-243546.
(UABR-) UAB RES FOUND.
Dillard JP, Yother J;
WPI; 96-010934/01.
New Streptococcus pneumoniae capsular polysaccharide genes - used for detection, serotyping and for diagnosis and prevention of S. pneumoniae infection
Disclosure; Page 178-180; 226pp; English.
Sequences encoding the 5' flanking region of the capsular polysaccharide gene (cps) of Streptococcus pneumoniae and which are of sufficient length to allow hybridisation under standard hybridisation conditions to a S. pneumoniae cps gene flanking region may be used in methods to detect and serotype S.pneumoniae. They may also be used for the diagnosis and prevention of S. pneumoniae
                                                                                                                                                                                                                                                                                                                                     Capsular polysaccharide of Streptococcus pneumoniae (CpsU).
Capsular polysaccharide; cps; peptide; flanking region; detection; serotype; diagnosis; prevention; Streptococcus pneumoniae.
Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligopeptide membrane transporter from Candida albicans and related nucleic acid - used to deliver therapeutic agents, especially antifungals, to target cells and to identify plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                        R83040 standard; peptide; 306 AA R83040;
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N-PSDB; V49601.
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07-FEB-1997; US-037859.
(UYTE-) UNIV TENNESSEE RES
Becker JM, Lubkowitz MA;
                                                                                                                                                                                              N-PSDB; T05848.
                                                                                                                                                                                                                                                                                                         23-NOV-1995
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659
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733
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50.0%;
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                          Matches
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                                 Best
                                                    infection.
Sequence
             67 yfdstfeley 76
                                 Local Similarity
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 YLSTSFSLDY
                          4;
                                                    306
                          Conservative
                                                    A
 12
                                 63.4%;
                                 Score 52;
Pred. No.
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                                 2.11e+02;
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Search completed: Thu Sep Job time: 20 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein · protein database search, using Smith-Waterman algorithm

n on: bular output not generated. Thu Sep 2 12:39:53 1999; MasPar time 4.71 Seconds 138.937 Million cell updates/sec

Description: Perfect Score: Title: >US-08-599-226-31 (1-12) from US08599226.pep 82 1 ASYLSTSFSLDY 12

Scoring table: •РАМ 150 Gap 15 Sequence:

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 25.125; Variance 38.161; scale 0.658

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

esult No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
<b>-</b>	63	76.8	372	5	P91143	SIMILAR TO ACETYLTRANS	6.49e-01
N	61		444	v	P91141	ТО	1.49e+00
w	59	٠	472	N	086563	TRANSMEMBRANE TRANSPOR	3.39e+00
4	59	72.0	1367	σı	Q20120	F44G4.8 PROTEIN (EC 3.	3.39e+00
ហ	56	68.3		N	Q55611		1.12e+01
0	55	67.1		σ	077768	HETEROGENEOUS NUCLEAR	1.65e+01
7	55	67.1		N	005237	HYPOTHETICAL 39.5 KD P	1.65e+01
8	55	67.1	360	œ	047575	CYTOCHROME B.	1.65e+01
9	55	67.1	603	œ	079437	NADH DEHYDROGENASE SUB	1.65e+01
10	54	65.9	84	ω	Q04203		2.43e+01
11	54	65.9	193	ω	Q12064	D1554.	2.43e+01
12	54	65.9	262	N	026039	CONSERVED HYPOTHETICAL	2.43e+01
13	54	65.9	316	N	065998	ORF36.	2.43e+01
14	53	64.6	389	თ	Q20272	COSMID F41C6.	3.56e+01
15	53	64.6	783	ω	014411	OPTIP.	3.56e+01
16	52	63.4	248	ш	059270	248AA LONG HYPOTHETICA	5.18e+01
17	52	63.4	253	N	P96151	DNA FOR AMINOPEPTIDASE	5.18e+01
18		63.4	265	10	024226	CHLOROPHYLL A/B BINDIN	5.18e+01
19		63.4	265	10	064442	LIGHT HARVESTING CHLOR	
20		63.4	336	N	047450	PAPG PROTEIN.	5.18e+01

45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	21
51	51	51	51	51	51	51	51	51	51	51	51	51	52	52	52	52	52	52	52	52	52	52	52	52
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POLYPROTEIN.	POLYPROTEIN.	POLYPROTEIN.	T25C12.3 PROTEIN.	HYPOTHETICAL PROTEIN T	XYLULOKINASE (XYLB).	PROTEIN	FAC	ELEG	25.9	.1 KD	T19C9.6 PROTEIN.	F8M12.8 PROTEIN.	SIMILAR TO S. POMBE IS	ATP SYNTHASE SUBUNIT I	GE E	HYPOTHETICAL 61.4 KD P	3	POTENTIAL-SENSITIVE PO	DNA POLYMERASE III ALP	CONSERVED HYPOTHETICAL	C41G6.7 PROTEIN.	PAPG PROTEIN.	PAPE.	PAPG PROTEIN.
7.50e+01	7.50e+01	7.50e+01	7.50e+01	7.50e+01		7.50e+01	7.50e+01	٠			•		5.18e+01	•	٠.	5.18e+01			٠.	•		5.18e+0	'n	5.18e+0

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Query Match	SEQUENCE 3	PFAM; PFOOS	EMBL; U883	WATERSTON R.;	STRAIN-BRISTOL N2;	SEQUENCE FROM N.A.	SUBMITTED	DAVIDSON S	STRAIN-BRISTOL N2;	SECTION OF PROM N A	NATURE 368	elegans.";		WATSON A.	THIERRY-MI	SMALDON N.	LIGHTNING	JONES M., I	GARDNER A.	CRAXTON M.,	BONFIELD J.,	WILSON R.	MEDLINE: 94150718.	SECONDERECTOR NO.	(T)	RHABDITINA	EUKARYOTA;	CAENORHABD:	C37H5.2.		01-MAY-1997	01-MAY-1997	P91143;	LT 1 P91143
76.8%; Score 63; DB 5; Length	372 AA; 42139 MW; 5214F159 CRC32;	PF00561; abhydrolase; 1.	TIED (FEB-1997) TO EMBL/GENBANK/DUBJ DATA BANKS U88315; G1825777;		ISTOL N2;	FROM N.A.	SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS	. ,	ISTOL N2;	FROM N A	NATURE 368:32-38(1994).			WEINSTOCK L. WILKINSON-SPROAT J. V	G J., THOMAS K., VAUDIN M., VAUGHAN	N., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN N., SMITH A., SONNHAMMER F., STADEN R., SHIRTON I		KERSHAW J.,		EAR S., D	CONNELL M., COPSEY T., CC	UGH R., ANDERSON K., BAYNES C.,	94150718.	FROM N.A.		RHĀBDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE	EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;	CAENORHABDITIS ELEGANS.	O ACELLULANDE ENABES.		(TREMBLREL. 03,	(TREMBLREL.		DRETIMINARY: DRET. 379 AA
rth 372;			KS.				iks.						omosome III of C.		K. WATERSTON R.	TRE D., SHOWNKEEN R.,	` `		M., JOHNSTON L.,		PER J., COULSON A.,	BERKS M.				PELODERINAE; CAENORHABDITIS.	IA; RHABDITIDA;			3				

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01-MAY-1997 (TREMBLREL. 03, LA
01-NOV-1998 (TREMBLREL. 08, LA
SIMILAR TO ACETYLTRANSFERASES.
C37H5.3.
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON I
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C
elegans.";
                  STREPTOMYCES COELICOLOR.

BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAB;
ACTINOMYCETALES; STREPTOMYCINEAB; STREPTOMYCETACEAE; ST
                                                                   01-NOV-1998 (TREMBLREL
01-NOV-1998 (TREMBLREL
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TRANSMEMBRANE TRANSPORT
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EUKARYOTA; METAZOA; NEMATODA;
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SEQUENCE 444 AA;
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DAVIDSON S., GILLAM |
SUBMITTED (FEB-1997)
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STRAIN-BRISTOL N2;
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MEDLINE; 94150718.
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SEQUENCE
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50.08;
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10
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08, LAST
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PROTEIN.
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Mismatches
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                       STREPTOMYCES.
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MURPHY L., HARRIS D
SUBMITTED (AUG-1998
[2]
SEQUENCE FROM N.A.
STRAIN-A3(2);
                                                                                       5
Q55611
Q5<sup>K</sup>
                                                           Q55611;
01-NOV-1996
01-NOV-1996
01-JAN-1999
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01-JAN-1999
01-AUG-1998
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Q20120;
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"A set of ordered cosmids and a d
the 8 Mb Streptomyces coelicolor
MOL. MICROBIOL. 21:77-96(1996).
EMBL; ALO31184; E1314374; -
SEQUENCE FROM N
STRAIN-PCC6803;
                         BACTERIA;
                                  SYNECHOCYSTIS
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                               SUBMITTED (SEP-1995) TO EMBL/G
EMBL; Z54218; E1346536; -.
EMBL; Z49910; E1346536; JOINED
                                                                                                                                                                                                                                                                                            CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                              F44G4.8 PROTEIN (EC F44G4.8.
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SEQUENCE 472
                                                    PROTEIN-EXPORT
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   RHABDITINA; RHABDITOIDEA;
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REDENBACH M., KIESER H.M.,
                                                                                                                                                  160 SYLODSFSIEY 170
                                                                                                                                                                                                                                                          HOMAS K.;
                                                                                                                                                                                                                                                                                                                                                                                                                     272 YLMTTFSLSY 281
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Similarity 70.0%;
7; Conservative
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(AUG-1998)
                       STIS SP. (STRAIN PCC CYANOBACTERIA; CHROC
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(AUG-1998) TO
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9 (TREMBLREL. 09, LAS'
8 (TREMBLREL. 07, LAS'
DTEIN (EC 3.1.3.48).
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63.6%;
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O EMBL/GENBANK/DDBJ
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01, LAST
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PROTEIN
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                        N PCC 6803).
CHROOCOCCALES;
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005237
005237;
01-JUL-1997
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                                                                                                                                                                                                              JIANG W., GUO X., BHAVANANDAN V.P.;
"Four distinct regions in the auxiliary domain nuclear ribonucleoprotein C-related proteins.";
BIOCHIM. BIOPHYS. ACTA 1399:229-233(1998).
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-NEW ENGLAND WHITE;
MEDLINE; 98438739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCG6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES: 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. sequence features in the 1Mb region from map positions 64% to 92% of the genome."; DNA RES. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                               ORYCTOLAGUS
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                                                                                                                                                                             NUCLEOPROTEIN;
SEQUENCE 306
                                                                                                                                                                                                                                                                                                                      LAGOMORPHA;
                                                                                                                                                                                                                                                                                                                                                                        HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96127529.
KANEKO T., TANAKA A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUGIURA M., TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 YLTIRFOLDY 164
                                                                                                  118 LSSSFDLDY 126
                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 YLSTSFSLDY
                                                                          4 LSTSFSLDY
                                                                                                                                                                            AF061582; G3660678; -.
OPROTEIN; RIBONUCLEOPROTEIN
NCE 306 AA; 33684 MW; FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D64000; D1010770;
NCE 315 AA; 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AUG-1995)
                                                                                                                                                                                                                                                                                                                                 METAZOA;
                                                                                                                                                                                                                                                                                                                               CUNICULUS (RABBIT).
METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                   (TREMBLREL. 08, (TREMBLREL. 08, (TREMBLREL. 08,
(TREMBLREL. 04, CREATED)
                                                                                                                                                                                                                                                                                                                    LEPORIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                         PRELIMINARY;
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                          12
                                                                                                                                       67.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SATO
                                                                                                                                                                                                                                                                                                                      ORYCTOLAGUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s.,
                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                        Score 55; DB 6; L
Pred. No. 1.65e+01;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 2;
Pred. No. 1.12e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOTANI H.,
                                                                                                                                                                             FBB28492 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4C20ED73 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                       357
                                                                                                                                                                                                                                                                                                                                                                                                                                      306 AA
                       Å
                                                                                                                                                                                                                                                                                                                                 MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAZUKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 315;
                                                                                                                           ۲.
                                                                                                                                                   Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ψ
                                                                                                                                                                                                                                          of heterogeneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T., MIYAJIMA
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                 EUTHERIA;
                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RA GHIMES, GUISEPPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENAUT A.,
RA GUISEPPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENAUT A.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA KOBAYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA KURITA K., LAPIUS A., LADINOIS S., MAUGEL C., MEDIGUE C.,
RA KURITA K., LAPIUS A., LIU H., MASUDA S., MAUGEL C., MEDIGUE C.,
RA KURITA K., PULIU H., MASUDA S., MAUGEL C., MEDIGUE C.,
RA KURITA K., JULI H., MASUDA S., MAUGEL C., MEDIGUE C.,
RA KURITA K., PORTETELLY M., OGAWA K., OGIWARA A., OUBEGA B., PARK S.H.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA MOONE D., O'REILLY M., OGAWA K., OGIWARA A., OUBEGA B., PARK S.H.,
RA ARRO V., POHL T.M., PORTETELLE D., PORWOLLIK S., PRESCOTT A.M.,
RA PRESECAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
RA SEKIGUCHI J., SEKOMSKA A., SEROR S.J., SERROR P., SHIN B.S.,
SOLDO B.,
RA SOROKIN A., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNANU A.,
RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNANU A.,
RA TAREUCHI M., WANBUTT R., WEDLER E., WEDLER H., WEITZENEGGER T.,
RA VIARI A., WANBUTT A., YAMAMOTO H., YAMANGE K., YASIMOTO K., YATA K.,
RA YOSHIDA K., YOSHIYAMA H. F., ZUMSTEIN R., VASIONOTO K., YATA K.,
RA YOSHIDA K., YOSHIYAMA H. F., ZUMSTEIN R., YANDANG K., YATA K.,
RA YOSHIDA K., YOSHIYAMA H. F., ZUMSTEIN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 98044033.

MEDLINE; 98044033.

MEDLINE; 98044033.

MEDLINE; 98044033.

MEDLINE; 98044033.

MEDLINE; 98044033.

MEDLINE; 98044033.

MEDLINE; 98044033.

MEDLINE COUNTIN A., BORCHERT S., BOLOTIN A., BORCHERT S., BRON S., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S., BRON S., BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., EMPON S., CAPURAN V., CARTER N.M., CHOIS. K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A., DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T., DENIZOT F., DEVINE K.M., DUSTERHOFT A., FERRARI E., FOULGER D., FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALLIZZI A., GALLERON N., FUJITA M., FUJITA Y., FUMA S., GALLIZZI A., GALLERON N., FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALLIZZI A., GALLERON N., FUJITA M., FUJITA M., GOLICHTLY E.J., GRANDI G., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YUGH.
BACTILIUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
PEAM; ELL PROHIBERT ST PROFILE STATE                                           EMBL; Z93934; E311527; -.
EMBL; Z9310; E118421B; -.
PROSITE; PE00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF0015; aminotran_1; 1.
PFAM; PF0015; prinotran_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 39.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                      KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDDJ DATA BANKS.
-I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KUNST F., OGASAWARA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE
                                                                                                                                                                                                                                                                                 AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (APR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (APR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APR-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-214 FROM N.A.
              Α,
              39461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.;
O EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GENBANK/DDBJ DATA BANKS
              MW;
              FD6B02F9
         CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterium Bacillus
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Query Match

Score 55;

DB

<u>ب</u>

Length

Ş В

 $\boldsymbol{\mu}$ 

ASYLSTSFSLDY SRYLSNRFDLSY Best Local Matches

75

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Query Match 67.1%;
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O79437 PRELIMINARY; P
O79437; PRELIMINARY; P
O79437; OR TREMBLREL 08, CRE
01-NOV-1998 (TREMBLREL 08, LAS
01-NOV-1998 (TREMBLEL 08, LAS
01-NOV-1998 TREMBLEL 08, LAS
01-NOV-1998 TREMBLEL 5.
                                                                                                                                                                                                      GENOMICS 50:161-169(1998).
EMBL; AJ001588; E1310026;
MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEDDIE E.M., UNNASCH T.R.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C =
FERROCYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOCHROME B. ONCHOCERCA VOLVULUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TREMBLREL. 01-JUN-1998 (TREMBLREL. 01-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION.
EUKARYOTA; METAZOA; NEMATODA;
FILARIOIDEA; ONCHOCERCIDAE; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORYCTOLAGUS CUNICULUS (RABBIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF015193; G2735939; -.
PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
MITOCHONDRION; ELECTRON TRANSPORT; RESPIRATORY CHAIN;
                                                                                                                                                                                                                                                                                                          "The complete mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: TWO HEME GROUPS
(B562 AND B566) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 50.0%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                    98317530.
, GULLBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                       67.18;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42544 MW;
                                                                                                                                                                                 67389
                                                                                                                                                                                                                                                                                                                                       ARNASON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96,
                                                                                                                                                                                   XX;
                                                                            Score 55;
Pred. No. 1
1; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55;
Pred. No.
4; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; SECERNENTEA; ONCHOCERCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
1; א
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                       u.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E80DD32E CRC32;
                                                                                                                                                                                   7A09A8C3
                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 1.65e+01; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 1.65e+01; Mismatches 1;
                                                                               Mismatches
                                                                                                       ; DB 8; Le
. 1.65e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
                                                                                                                                                                                   CRC32;
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Q04203;
AC Q04203;
AC Q04203;
AC Q04203;
AC Q04203;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE HYPOTHETICAL PROMISER

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RESQUENCE FROM N.A.

RC STRAIN-AB972;
RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
RC STRAIN-AB972;
RA BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
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AC Q1

RESULT 12
ID 026039
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012064;
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01-NOV-1996
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DELAVEAU
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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI: ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                          SUBMITTED (JUL-1996) TO EMEMBL; X97751; E242701; -... EMBL; Z74199; E253062; -... SEQUENCE 193 AA; 20893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
PEREA J., BLUGEON C.
SUBMITTED (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED
                                                                                                                                 149 FLATAFGLNF 158 : |:|:|:|:|:
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Local Similarity 60.0%;
les 6; Conservative
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J T., BLUGEON (
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TO EMBL/GENBANK/DDBJ
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EMBL/GENBANK/DDBJ
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2; Mismatches
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Pred. No. 2.
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HEME. SEQUENCE

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SEQUENCE FROM N.A. MEDLINE; 98317530. GISSI C., GULLBERG

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01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
CONSERVED HYPOTHETICAL IN
14
Q20272
Q20272;
Q20272;
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01-NOV-1998
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01-AUG-1998
01-AUG-1998
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TOMB J.-F., WHITE O., KETCHUM K.A., KLANKH.-P., GILL S., DOUGHERTY B.A.

FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.

NELSON K., OUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,

LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,

MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,

BERG D.E., GCCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.

COTTON M.D., WEIDMAN J.M., FUJII C., BOMMAN C., WATTHEY L., WALLIN

HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,

VENTER J.C.;
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HYPOTHETICAL PROTEIN.
262 AA; 28835
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25;389(6649):412].";
NATURE 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                        BEHRENS S.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA
EMBL; U58131; G3025464; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLOSTRIDIUM.
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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(TREMBLREL.
(TREMBLREL.
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                                                                                      PRELIMINARY;
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OTEOBACTERIA; EPSILON SUBDIVIS
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. 05, LAST SEQUENCE UPDATE)

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INTEGRAL MEMBRANE PROTEIN.
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d. No. 2.43e+01;
Mismatches 3;
SEQUENCE UPDATE)
ANNOTATION UPDATE)
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"An oligopeptide transport g
MICROBIOLOGY 143:0-0(0).
EMBL; U60973; G2367386; -.
SEQUENCE 783 AA; 88406 MW
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014411;
01-JAN-1998
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BONFIELD J., BURTON J., CONNELL M., COPERY J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FRAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (OCT-1995) TO EMBL; U39745; G1049476; SEQUENCE 389 AA; 442
                                                                                                                                                                                                                                                                                               STRAIN=1006;
MEDLINE; 971
                                                                                                                                                                                                                                                                                                                                                                                                         CANDIDA ALBICANS (YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA;
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MEDLINE; 94150718.
WILSON R., AINSCOUGH R.,
BONFIELD J., BURTON J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHAE
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Search completed: Thu Job time: 30 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Sep 2 12:39:25 1999; MasPar time 2.20 Seconds 154.427 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-599-226-31 (1-12) from USO8599226.pep 82 1 ASYLSTSFSLDY 12

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Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 I:swissprot

Statistics: Mean 26.265; Variance 33.740; scale 0.778

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

esult No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
٦	63	76.8	272	¦	YIGL_HAEIN	HYPOTHETICAL PROTEIN H	1.04e-01
2	62	75.6	1294	ب		149.2 KD	1.67e-01
ω	57	9	296	μ	CYCG_RHOSH	HROME C	1.69e+00
4	57	69.5	300	ш	GP40_HUMAN	PUTATIVE G PROTEIN-COU	٠
ഗ	56	8	575	1	CNGX_RAT	CYCLIC-NUCLEOTIDE-GATE	2.64e+00
o	ហ	7.	303	щ	ROC_HUMAN	HETEROGENEOUS NUCLEAR	٠
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00	S	7	445	<b>ب</b>	ACSC_MOOTH	CORRINOID/IRON-SULFUR	4.10e+00
9	54	.5	277	μ.	ICE3_CRILO	APOPAIN PRECURSOR (EC	6.33e+00
10	54		277	ш	ICE3_RAT	APOPAIN PRECURSOR (EC	
11	54	5	277	μ	ICE3_MOUSE	PRECURSOR (	
12	54	5	611	μ	YCR3_YEAST	HYPOTHETICAL 69.2 KD P	•
13	υs		175	μ	RL6B_YEAST	60S RIBOSOMAL PROTEIN	
14	5ω		175	۳	RL6A_YEAST	60S RIBOSOMAL PROTEIN	٠
15	53	64.6	324		GSHB_ANASP	GLUTATHIONE SYNTHETASE	•
16	53		738	ш	ST11_YEAST	SERINE/THREONINE-PROTE	9.73e+00
17	52	63.4	122	L	YG27_YEAST	HYPOTHETICAL 14.4 KD P	•
18	52	63.4	180	1	APT_MASHI	ADENINE PHOSPHORIBOSYL	•
19	52	63.4	180	1	APT_STOLO	ADENINE PHOSPHORIBOSYL	1.49e+01
20	52	63.4	227	щ	PGSA_MYCPN	CDP-DIACYLGLYCEROLGL	1.49e+01
21	52	63.4	306	_	CAPC_STRPN	UTPGLUCOSE-1-PHOSPHA	1.49e+01
22	52	63.4	428	<u>_</u>	YE63_SCHPO	HYPOTHETICAL 48.7 KD P	1.49e+01
23	52	63.4	475	Н	YM61_YEAST	HYPOTHETICAL 55.3 KD P	•

4 4 5 4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	•	62.2	62.2	62.2
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MCEL_VARV	FASD_ECOLI	CAOQ_RAT	SYR_HAEIN	GUNB_RUMAL	GUN1_RUMAL	CB23_PETSP	ATP6_RHORU	APT_HELPY	POLG_DEN1S	TGLK_RABIT	TGLK_RAT	TGLK_HUMAN	AFSK_STRGR	AFSK_STRCO	LCNC_LACLA	YR47_CAEEL	CYHR_CANMA	CB23_POLMU	YB9L_YEAST	VG87_BPML5
MRNA CAPPING ENZYME, L	OUTER MEMBRANE USHER P	PRISTANOYL-COA OXIDASE	ARGINYL-TRNA SYNTHETAS	ENDOGLUCANASE B PRECUR	ENDOGLUCANASE I PRECUR	CHLOROPHYLL A-B BINDIN	ATP SYNTHASE A CHAIN (	ADENINE PHOSPHORIBOSYL	GENOME POLYPROTEIN [CO	PROTEIN-GLUTAMINE GAMM	PROTEIN-GLUTAMINE GAMM	PROTEIN-GLUTAMINE GAMM	SERINE/THREONINE PROTE	SERINE/THREONINE PROTE	LACTOCOCCIN A TRANSPOR	HYPOTHETICAL 66.0 KD P	CYCLOHEXIMIDE RESISTAN	CHLOROPHYLL A-B BINDIN	HYPOTHETICAL 16.0 KD P	GENE 87 PROTEIN (GP87)
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# ALIGNMENTS

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Query Match	EMBL; U3 TIGR; HI PROSITE; PROSITE; PFAM; PF HYPOTHET SEQUENCE	This SWIS between the Europ use by modified entities or send a	"Whole-gencinfluenzae SCIENCE 269 -!- SIMILAI (B.SUB)	UTTERBAC FINE L.D GNEHM C. VENTER J	STRAIN-R MEDLINE; FLEISCHM FLEISCHM KERLAVAG KERLAVAG MCKENNEY SCOTT J. SCOTT J.	HAEMOPHILUS BACTERIA; PR HAEMOPHILUS. [1] SEQUENCE FRO	01-NOV-1995 01-NOV-1995 01-OCT-1996 HYPOTHETICAL	TT 1 YIGL_HAEIN P44771:
	EMBL: U32741; G1573586; TIGR; H10597; PROSITE; PS01228; COF_1; 1 PROSITE; PS01229; COF_2; 1 PFAM; PF00592; DUF3; 1. HYPOTHETICAL PROTEIN. SEQUENCE 272 AA; 30523	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."; SCIENCE 269:496-512(1995)i- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (E.COLI) / (B.SUBTILIS) FAMILY. STRONG, TO E.COLI YIGL.	UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEEM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.;	STRAIN-RD / KW20;  MEDLINE; 95350630,  FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., MERRICK KERLAVAGE A.R., BULT C.J., TOMB JF., DOUGHERTY B.A., MERRICK MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU LT., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.	HAEMOPHILUS INFLUENZAE. HAEMOPHILUS INFLUENZAE. BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; HAEMOPHILUS. [1] SEQUENCE FROM N.A.	٢,,,,	
76.8%;	73586; COF_1; 1. COF_2; 1. F3; 1. EIN. 30523 MW;	Institute formatics t institutes t institutes t institus statement a license o license o	om sequenc 2(1995). LONGS TO TRAMILY. STR	NNA M.C., AN J.L., F LD L.A., S	ADAMS M.D. LT C.J., T N G., FITZ Y R., LIU LIPS C.A.,	NZAE. CTERIA; GA	REL. 32, CREATED) REL. 32, LAST SEQ REL. 34, LAST ANN PROTEIN HI0597.	STANDARD;
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Length 272;	1	roduced through a collaboration ics and the EMBL outstation - re are no restrictions on its as its content is in no way Usage by and for commercial http://www.isb-sib.ch/announce/	Haemophil	D.M., BRAI AGEN N.S.M .M., SMITH	M.D., WHITE O., CLAYTON R.A., KIRK I., TOMB JF., DOUGHERTY B.A., MER FITZHUGH W., FIELDS C.A., GOCAYNE LIU LI., GLODEK A., KELLEY J.M., I.A., SPRIGGS T., HEDBLOM E., COTTO	PASTEURELLACEAE;		
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HYPOTHETICAL 149.2 KD PROTEIN C18B11.11 IN CHROMOSOME
SPAC18B11.11 OR SPAC1F5.01.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI, ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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MEDLINE; 9:
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                                                                                                                                                                       FLORY J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
01-NOV-1997
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PROM; PF00001; 7tm_1; 2.
PFAM; PF00001; 7tm_1; 2.
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                "A cluster of four novel human G protein-coupled receptor genes occurring in close proximity to CD22 gene on chromosome 19q13.1."; BIOCHEM. BIOPHYS. RES. COMMUN. 239:543-547(1997).
-i- FUNCTION: ORPHAN RECEPTOR.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                 EMBL; AF024687; G2612946; GCRDB; GCR_2538; -.
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SUBCELLULAR LOCATION: MEMBRANE-BOUND:
PTM: BINDS TWO HEME GROUPS PER MOLECULE (POTENTIAL).
SIMILARITY: TO ACETOBACTER ALCOHOL DEHYDROGENASE CYTOCHROME
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDAT
CYCLIC-NUCLEOTIDE-GATED OLFACTORY CHANNEL O
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; METAZOA; CHORDATA; METAZOA; CH
                   use by modified
                                                      the
                                                                                                                                                                                   BRADLEY J., ZHANG Y., BAKIN R., LESTER H.A., RONNETT G., ZINN K.;
SUBMITTED (DEC-1996) TO EMBL/GENERAL TRANSAUCTION IS PARKABLY
-!- FUNCTION: ODDERANT SIGNAL TRANSAUCTION IS PROBABLY MEDIATED
BY A G-PROTEIN COUPLED CASCADE USING CAMP AS SECOND MESSENGER.
THE OLFACTORY CHANNEL CAN BE SHOWN TO BE ACTIVATED BY CYCLIC
NUCLEOTIDES WHICH LEADS TO A DEPOLARIZATION OF OLFACTORY
SENSORY NEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRADLEY J., LI J., DAVIDSON N., LESTER H.A., ZINN K.; "Heteromeric olfactory cyclic nucleotide-gated channels: that confers increased sensitivity to cAMP."; PROC. NATL. ACAD. SCI. U.S.A. 91:8890-8894(1994).
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                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the El European Bioinformatics Institute. There are no rest
                                                                                                                         SUBUNIT: HETEROOLIGOMER OF OCNC1 AND C
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MEDLINE; 87257872.
MEDLINE; 87257872.
SWANSON M.S., NAKAGAWA T.Y., LEVAN K., DREYFUSS G.;
Primary structure of human nuclear ribonucleoprotein particle proteins: conservation of sequence and domain structures in heterogeneous nuclear RNA, mRNA, and pre-rRNA-binding proteins heterogeneous nuclear RNA, mRNA, mRNA, and pre-rRNA-binding proteins heterogeneous nuclear RNA, mRNA, mRN
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PARTIAL SEQUENCE, AND CHARACTERIZATION. MEDLLNE; 90067819.
MERRILL B.M., BARNETT S.F., LESTOURGEON "Primary structure differences between nuclear ribonucleoprotein particles."; NUCLEIC ACIDS RES. 17:8441-8449(1989).
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01-AUG-1991 (REL. 19,
01-FEB-1995 (REL. 31,
HETEROGENEOUS NUCLEAR
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; CAMP-BINDING; TRANSMEMBRANE;
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H2 (POTENTIAL)
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H1 (POTENTIA
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P (POTENTIAL).
P (POTENTIAL).
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                                                    proteins
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s nuclear rib
RNA binding
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EMBL; M16342; G306875; -.
PIR; C34504; C34504.
PIR; A26885; A26885.
AARHUS/GHENT-2DPAGE; 7207; I
AARHUS/GHENT-2DPAGE; 7222; I
                                                                            SHIA_ECOLI STANDARD; rat, ....
P76350:
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
SHIKIMATE TRANSPORTER.
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STRUCTURE
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SEQUENCE
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SEQUENCE FROM N.A. STRAIN~K12;
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                                      BACTERIA; PI
ESCHERICHIA
                                                                 ESCHERICHIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOERLACH M., WITTEKING M., BECKMAN R.A., MUELLER L., DREYFUSS "Interaction of the RNA-binding domain of the hnRNP C proteins
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                                                                                                                                                                                                                                         118 LSSSFDLDY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MAY PLAY A ROLE IN RIBONUCLEOSOME ASSEMBLY BY NEUTRALIZING BASIC PROTEINS SUCH AS A AND B CORE HURNP.
SUBCELLULAR LOCATION: NUCLEAR: COMPONENT OF RIBONUCLEOSOM
PTM: PHOSPHORYLATED (PROBABLE).
ALTERNATIVE PRODUCTS: C1 AND C2 PROTEINS PROBABLY RESULT
ALTERNATIVE SPLICING OF THE PRE-WRNA. C2 IS IDENTICAL TO
EXCEPT FOR AN INSERT OF 13 AA (AA 108-120) ONLY PRESENT I
SIMILARITY: HIGH, TO X.LAEVIS PROTEIN C.
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PS00030; RNP_1; 1.
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                                                    GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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Pred. No. 4.10e+00;
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MISSING (IN HNRNP C1).
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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CORE HNRNP.
RIBONUCLEOSOMES.
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A ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., A ITOH T., AIBA H., KIMURA S., KITAKAWA M., KITAGAWA M., A ISONO K., KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M., A MAKINO K., MIKI T., MIZOBUCHI K., WORI H., MORI T., OSHIMA T., A NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., A SAITO N., SAMPEI G., SEKI Y., SIVASUDARAM S., TAGAMI H., A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WATA M., WATA M., TAKAMOTO Y., HORIUCHI T.; A TAKEDA J., TAKEMOTO K., WATA M.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKE
ACSC_MOOTH
Q07340;
Q1-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RILEY M., CCLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F. GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
"The complete genome securation"
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SEQUENCE
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WHIPP M.J., CAMAKARIS H., PITTARD A.J.;
"Cloning and analysis of the shiA gene, which encodes the shikimate transport system of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D90837;
ECOGENE; EG20;
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TE; PS00217; SUGAR_TRANSPORT_2;
PF00083; sugar_tr; 1.
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AE000290; G178829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L07099; G144854; -. PIR; A46621; A46621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (REL. 31, 15-DEC-1998 (REL. 37, CORRINOID/IRON-SULFUR
SEQUENCE FROM
TISSUE-BRAIN;
                                                                                                                CRICETULUS LONGICAUDATUS (LONG-TAILED HAMSTER) (CHINESE HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOORELLA.
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                                                                                       RODENTIA;
                                                                                                                                                                                 CASP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [NIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 YVTTNESLTY 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YLSTSFSLDY 12
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SUBUNIT: HETERODIMER OF A LARGE AND SMALL CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A46621; A46621.
P01088; 1BFA.
                                                                                                                                                                              OR CPP32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 60.0% 6; Conservative
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                                                                                       SCIUROGNATHI;
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                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                             35, CARRATED)
35, LAST SEQUENCE UPDATE)
36, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
(EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLOSTRIDIUM THERMOACETICUM)
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                                                                                       MURIDAE;
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ANNOTATION UPDATE)
EIN, LARGE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 1; L
Pred. No. 4.10e+00;
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IRON-SULFUR (4FE-45) (PROBABLE).
IRON-SULFUR (4FE-45) (PROBABLE).
FAGACBC6 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                          CRICETINAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 445;
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                                                                                         ICE3_RAT STANDARD; PRT; 277 AA.

p55213; p70543; 062993; p97699;

01-OCT-1996 (REL. 34, CREATED)

01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL. 35, LAST SNOTATION UPDATE)

APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32)

PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREHP CLEAVAGE ACT

(SCA-1) (LICE) (IRP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPP32 during apoptosis.";
EMBO J. 15:1012-1020(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
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use
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                                                                 RATTUS NORVEGICUS (RAT)
                                                                                  CASP3 OR CPP32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96183185
WANG X., ZELENSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS I PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOPHELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN. CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY). SUBUNIT: HETERODIMER OF A 17 KD (P17) AND A 12 KD (P12) SUBUNIT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: CYTOPLASMIC.

SYBCELLULAR LOCATION: CYTOPLASMIC.

PYM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE PYMORE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES THO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR PACE VERSA (BY SIMILARITY).

SYMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE CASPASE FAMILY.
                                                                                                                                                                                                                                              YLSTSFSLDY
  FROM N.A.
96358624.
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                                          SCIUROGNATHI;
                                                      METAZOA;
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                                                      CHORDATA;
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                                          MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                ZYMOGEN; APOPTOSIS.
BY SIMILARITY.
BY SIMILARITY.
APOPAIN P17 SUBUNIT.
APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                              Score 54; DB 1; Pred. No. 6.33e+00
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:
                                        VERTEBRATA;
AE; MURINAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no rest
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                                          MAMMALIA;
RATTUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                         Length 277;
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                                                                                                          32) (YAMA
ACTIVITY
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EMBL; U49930; G1518936; -.
EMBL; U34685; G1004371; -.
EMBL; U84410; G1814027; -.
EMBL; U86566; G1381643; -.
EMBL; U58656; G1381643; -.
PROSITE; PS01121; CASPASE_CYS; 1
PROSITE; PS01122; CASPASE_CYS; 1
PROM; PF00655; ICE_P10; 1.
PFAM; PF00655; ICE_P20; 1.
HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLAWS J.A., KUGU K., TRBOVICH A.M., DESANTI A., TILLY K.I., HIRSHFIELD A.N., TILLY J.L.;
"Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa ce of the ovarian follicle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUAN T.S. FLETCHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme (ICE)-related protease (IRP) and its possible role
apoptosis of cultured cerebellar granule neurons.";
J. NEUROSCI. 17:1561-1569(1997).
                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
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ROSTECK P. JR., POIRIER G.G., PAUL S.M.;
"Cloning and expression of a rat brain interleukin-lbeta-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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        HYDROLASE;
                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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-!- FUNCTION: INVOLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADULT BRAIN.

PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES TO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPERTIDES LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CP932 ALSO OCCUR FUCE VERSA (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT PROTEOLYCITCALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-HELIX LEUGINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN. CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY). SUBUNIT: HETERODIMER OF A 17 KD (P17) AND A 12 KD (P12) SUBUNIT
                                                                                                                                                                                                                                                                                                                                                              ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAI
BUT NOT IN KIDNEY OR TESTIS.
DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEU
OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CASPASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                     requires a license agreement (Some mail to license@isb-sib.ch).
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1PAU.
IOL PROTEASE;
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     APOPTOSIS
                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
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"Specific expression c
activation of CPP32 in
NGF.";
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P70677; O08668;
01-NOV-1997 (RE)
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FERNANDES-ALNEMRI T., LITWACK G., ALNEMRI E.S.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (NAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CARESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET
                                                            FEBS
                                                                                                   STRAIN-C3H/AN;
STRAINE; 97190206.
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EUKARYOTA; METAZOA; CHORDATA;
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                                   TISSUE-BRAIN;
                                                                    Characterization
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                                            EQUENCE
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3 YLSTSFSLDY 12
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403:61-69(1997).
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                                                                                             VANDENABEELE
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(BC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY
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n of CPP32 in sensory neurons of mouse embry
in the apoptosis induced by a withdrawal of
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LAST SEQUENCE UPDATE)
                                                                                                                                       COMMUN. 231:770-774(1997)
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APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
APOPAIN P17 SUE
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AE; MURINAE;
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          CASPASES
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EMBL; U54802; G1518968; JOINED.
EMBL; U49929; G1518934; -...
EMBL; D86352; G1945544; -...
EMBL; D86352; D1022582; -...
EMBL; V13086; E315505; -...
EMBL; V19522; G2114328; -...
EMBL; U19522; G2114328; -...
MGD; MGI:107739; CASP3
ILT 12
YCR3_YEAST
P25351;
01-MAY-1992
01-MAY-1992
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PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERAL

PTM: ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTI

LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED

PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF

CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCC
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TISSUE SPECIFICITY: HIGHEST EXPRESSION
KIDNEY AND HEART. LOWER EXPRESSION IN E
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larity 50.0%;
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Mismatches 2;
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Best I
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STRAIN-S288C / AB972;
JOHNSTON M., ANDREWS S., BR
FAVELLO A., FULTON L., GATT
KUCABA T., HALLSWORTH K., H
JOHNSON D., JOHNSTON L., LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S19434;
PIR; S22273;
HYPOTHETICAL
TRANSMEM
TRANSMEM 1
TRANSMEM 2
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SEQUENCE
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HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMF1 INTE
YCR023C OR YCR23C OR YCR241.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                  MEDLINE; 9
                                                                                                                                                                                  01-NOV-1988 (REL. 09, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
60S RIBOSOMAL PROTEIN L6-B (L17) (YL16) (RP18).
RPL6B OR YL16B OR RPL16B OR YLR448W OR L9324.4.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
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                                                                               HASHIMOTO T., SUZUKI K., MIZUTA K., OTAKA E., "Yeast ribosomal proteins: XIV. Complete nucleotide two genes encoding Saccharomyces cerevisiae YL16."; BIOCHIM. BIOPHYS. ACTA 1132:195-198(1992).
                                                                                                                                        SEQUENCE
                                                                                                                                                               SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                  RL6B_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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YEAST 8:205-213(1992).
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Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced througen the Swiss Institute of Bioinformatics and the
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PROTEIN;
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                      GATTUNG
  LANGSTON Y
                                   BRINKMAN R.,
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  ¥.,
 R., COOPER J., DIN
, GRECO T., KIRSTEN
J., HILLIER L., JI
Y., LATREILLE P.,
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kb fragment between
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                      KIRSTEN
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Matches 7; Conse
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EMBL; U22382; G717063; -.
PIR; S11257; S11257.
PIR; S28945; S28945.
SGD; L0001714; RPL6B.
                                                                                                                                                                                                                                                                                                                                                        01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANOTATION UPDATE)
60S RIBOSOMAL PROTEIN L6-A (L17) (YL16) (RP18).
RPL6A OR YL16A OR YML073C.
                                                                                                                                                                                                                                                                                                                                                                                                                                          RL6A_YEAST
Q02326;
                                                                             STRAIN-S288C / AB972;
BROWN D., BOWNAN S., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (CCT-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- THERE ARE TWO GENES FOR L6 IN YEAST.
-!- SIMILARITY: BELONGS TO THE L6E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RIFKEN
WILCOX
                                                                                                                                                                                                                                                                                                                           SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMY
                                    between
                                                    This
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 93003323.
HASHIMOTO T., SUZUKI K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTAKA E., HIGO K.-I., ITOH T.;
"Yeast ribosomal proteins: VIII. Isolatic sequence characterization of twenty-four
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                             HASSHIMOTO T., SUZUKI K., MIZUTA K., OTAKA E., 
"Yeast ribosomal proteins: XIV. Complete nucleotide sequences two genes encoding Saccharomyces cerevisiae YL16."; 
BIOCHIM. BIOPHYS. ACTA 1132:195-198(1992).
                                                                                                                                                                                                                                                                                                               SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01170; RIBOSOMAL_L6E; 1.
PFAM; PF01159; L6e; 1.
RIBOSOMAL PROTEIN; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOL. GEN. GENET. 195:544-546(1984).
-!- THERE ARE TWO GENES FOR L6 IN YEAST.
-!- SIMILARITY: BELONGS TO THE L6E FAMILY OF RIBOSOMAL PROTEINS.
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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175
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larity 87.5%;
Conservative
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EMBL; Z46373; G914877; -.
PIR; S28944; S28944.
SGD; L0004165; RPL6A.
PROSITE; PS01170; RIBOSOMAI
PFAM; PF01159; L6e; 1.
                                                                                                                GLUTATHIONE
CONFLICT
CONFLICT
                                                                                                                                                                               EMBL; U14408;
EMBL; Z31371;
HSSP; P04425;
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ZHANG C.C., HUGUENIN S., FRIRY A.;

"Analysis of genes encoding the cell division protein FtsZ and glutathione synthetase homologue in the cyanobacterium Anabaena PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P45480; Q43879;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
CLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cyanobacterium Anabaena GENE 163:93-96(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHETASE)
                                                                                           SEQUENCE
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DOHERTY H.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    . MICROBIOL. 146:445-455(1995).

CATALYTIC ACTIVITY: ATP + GAMMA-L-GLUTAMYL-L-CYSTEINE
ADP + ORTHOPHOSPHATE + GLUTATHIONE.

PACHWAY: SECOND STEP IN GLUTATHIONE BIOSYNTHESIS.

SIMILARITY: TO OTHER PROKARYOTIC GSH SYNTHASES.
  Similarity
5; Conse
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96099685.
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243
324 AA;
                                                                                                                                                            BIOSYNTHESIS;
                                                                                                                                                                          ; E190151; -. ; 2GLT.
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larity 45.5%;
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C -> W (IN REF. 2
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61CCOD40 CRC32;
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                       DB 1; L
9.73e+00;
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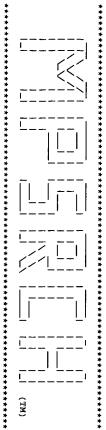
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Ş B 102 AYLYATYVLDY 112 :|| ::: ||| 2 SYLSTSFSLDY 12

Search completed: Thu Sep 2 12:39:34 1999 Job time : 9 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: bular output not generated. Thu Sep 2 12:38:52 1999; MasPar time 3.15 Seconds 152.742 Million cell updates/sec

Title:

Sequence: Description: Perfect Score: >US-08-599-226-31 (1-12) from US08599226.pep 82 1 ASYLSTSFSLDY 12

Scoring table: PAM 150 Gap 15

Searched:

122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

l:pirl 2:pir2 3:pir3 4:pir4

Mean 25.698; Variance 36.778; scale 0.699

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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genome polyprotein -	hypothetical protein	protein-glutamine gam	ATP-dependent membran	cycloheximide resista	protein-glutamine gam	conserved hypothetica	ř	gene 87 protein - Myc	DNA-directed DNA poly	probable ATP synthase	probable PE protein -		DNA-directed DNA poly	hypothetical protein	conserved hypothetica	adhesin p		protein		_	hypothetical protein
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# ALIGNMENTS

RESULT 2 ENTRY TITLE	Db 261 ARYLRTQFGLDY	Query Match Best Local Similarity Matches 8; Conse	CLASSIFICATION SUMMARY	##note	##residues ##cross-referen	##status	#cross-referent #accession	#title	#iournal							#authors	REFERENCE	ACCESSIONS	ORGANISM DATE	TITLE	RESULT 1 ENTRY
<pre>S58307  #type complete hypothetical protein SPAC18B11.11 - fission yeast (Schizosaccharomyces pombe)</pre>	ARYLRTQFGLDY 272          :    ASYLSTSFSLDY 12	76.8%; Score 63; DB 2; Length 272; ilarity 66.7%; Pred. No. 3.53e-01; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	*superfamily hypothetical protein HI0597 #length 272 #molecular-weight 30523 #checksum 8761	best homolog was a hypothetical protein from Escherichia	ces	nucleic acid sequence not shown; translation not shown	#cross-references MUID:95350630 #accession D64155	Whole-genome random sequencing and assembly of Haemophilus	Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.	Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L	M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,	J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,	shirley R.: Liu I.I. Glodek A. Kelley J.M.: Weidman.	Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;	<pre>Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;</pre>	Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;	A64000	10 Sep 1330 D64155	#formal_name Haemophilus influenzae #Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-50-1000	hypothetical protein H10597 - Haemophilus influenzae (strain Rd KW20)	D64155 #type complete

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RESULT
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##residues 1-1294 ##label DEV
##cross-references EMBL: Z50728; NID: g929886;
                                                                                                                                                                       105 YLGAAFPLGY 114
                                                                                                                                                                                                 69.5%;
Local Similarity 50.0%;
hes 5; Conservation
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##cross-references GB:AF024687; NID:g2612945; PID:g2612946
glycoprotein; lipoprotein; thiolester bond
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#type complete
hypothetical protein - Synechocystis
#formal_name Synechocystis sp.
PCC 6803
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Jr., L.F.; O'Dowd, B.F.
Blochem. Blophys. Res. Commun. (1997) 239:543-547
A cluster of four novel human G protein-coupled receptor
genes occurring in close proximity to CD22 gene on
chromosome 19413.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Devlin, K.; Churcher, C.M. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JC5714
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14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
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4.54e+00;
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                                                                                                                                                                                                                                                         #title A second subunit of the olfactory cyclic nucleotide-gated channel confers high sensitivity to cAMP.

#cross-references MUID:95000663

#accession 158165
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#accession I59327
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##cross-references EMBL:U12425; NID:g548083; PID:g548084
##CICATION #superfamily CAMP receptor protein cyclic nuc
                                                                                                                                                                                                                 **scatus preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
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##residues 1-31
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PID:g1001494
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Local Similarity 60.0%;
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DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence and Sequence and Sequence and Sequence and Sequence Synechocystis sp. PCC6803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradley, J.; Li, J.; Davidson, N.; Lester, H.A.; Zinn, K. Proc. Natl. Acad. Sci. U.S.A. (1994) 91:8890-8894 Heteromeric olfactory cyclic nucleotide-gated channels: A new subunit that confers increased sensitivity to cAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159327 #type complete
olfactory cyclic nucleotide gated cation channel - rat
#formal_name Rattus norvegicus #common_name Norway rat
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
#length 315 #molecular-weight 34667 #checksum 4918
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Neuron (1994) 13:611-621
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Nakamura, Y.; Miyajima, N.; Hiosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo,
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domain homology #label CA2
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Pred. No. 6.85e+00
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No.
  DB 2; L
6.85e+00;
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#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:9788-9792
#title Primary structures of the heterogeneous nuclear
ribonucleoprotein A2, B1, and C2 proteins: a diversity of
RNA binding proteins is generated by small peptide inserts.

#cross-references MUID:90099350
#accession C34504
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##CIGATION #superfamily unassigned ribonucleoprotein repe
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Runst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursler, L.; Brans,
A.; Brann, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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#formal_name Homo sapiens #common_name man
22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change
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#cross-references MUID:98044033
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                                                                                                                                                                                                                                                                                                                                                             ##residues 1-438 ##label BLAT ##cross-references GB:AE000290; GB:U000096; NID:g2367125;
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##cross-references GB:Z99120; GB:
##cross-references EMBL:U88529
                                                                                                                                                                                                                                                                                                            ##experimental_source strain K-12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##experimental_source strain 168
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Nature (1997) 390:249-256
                                                                                                                                                 Whipp, M.J.; Camakaris, H.; Pittard, A.J. Gene (1998) 209:185-195 of the shiA gene, which encodes the Cloning and analysis of the shiA gene, which encodes the shikimate transport system of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science (1997) 277:1453-1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily aspartate transaminase #length 357 #molecular-weight 39461 #checksum
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#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shikimate transport
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  translation not shown
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                             1-438 ##label WHI
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Pred. No. 1.03e+01
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58-76
96-114
117-135
171-189
198-216
260-278
291-309
319-337
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J. W.F.; Schiau, I.; Cunningham, J.R.; Ragsdale, S.W.
J. Biol. Chem. (1993) 268:5605-5614

#title Sequence and expression of the gene encoding the
corrinoid/iron-sulfur protein from Clostridium
thermoaceticum and reconstitution of the recombinant
protein to full activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##note
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YLSTSFSLDY
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C/Fe-Sp large chain AcsC

#formal_name Clostridium thermaceticum
21-Sep-1993 #sequence_revision 04-Oct-
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aromatic amino acid biosynthesis
#superfamily citrate utilization determinant
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4Fe-4S; carbon dioxide fixation; electron transfer;
heterodimer; iron-sulfur protein; metalloprotein
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A46621
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larity 60.0%;
Conservative
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sequence extracted
NCBIP:127878)
                                                                                                                                                                                                                                                                  #binding_site 4Fe-4S cluster (Cys) (covalent) #status
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#status experimental #label MAT\
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                                                                                                              Score 55; DB 1; Pred. No. 1.03e+01;
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Pred. No. 1.03e+01;
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RESULT

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Best Local Similarity 60.0%;
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##cross-references EMBL:249919; ]
                                                                                                                                                          149 FLATAFGLNF 158
                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:274199; NID:g1431236; MIPS:YDL151c
                                                                                                                                                                                                                                                                                                                                       ##experimental_source strain
                                                                                                                                                                                                                                                                                                                                                                                   ##residues
                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
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                                                                                                                                3 YLSTSFSLDY 12
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                                                                                                                                                                                                                                                                                                                                                                                                            Perea, J.; Blugeon, C.; Delaveau, T.; Jacq, submitted to the Protein Sequence Database, 867699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein D1554

#formal_name Saccharomyces cerevisiae
12-Jul-1996 #sequence_revision 12-Jul-1996
14-Nov-1997
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S57541
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#formal_name Saccharomyces cerevisiae
10-Oct-1995 #sequence_revision 03-Nov-1995
21-Nov-1997
            cysteine proteinase (EC 3.4.22.) p32 -
#formal_name Rattus norvegicus #common_n
26-yul-1996 #sequence_revision 26-yul-19
_17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S57545 #type complete probable membrane protein YPR012w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                  #length
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                                                                       #type fragment
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                                                                                                                                                                                       Score 54; DB 2;
Pred. No. 1.53e+01
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 2; L
Pred. No. 1.53e+01;
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                         .-) P32 - rat (fragment) #common_name Norway rat 26-Jul-1996 #text_change
                                                                                                                                                                                                                  Length 193;
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#checksum 7108
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ORGANISM DATE RESULT ENTRY TITLE RESULT ENTRY ş #gene CLASSIFICATION GENETICS S 밁 SUMMARY REFERENCE #authors ORGANISM KEYWORDS TITLE ACCESSIONS REFERENCE Matches Query Match 65.9%; Best Local Similarity 58.3%; Query Match
Best Local Similarity #journal #title #journal Nature (1999) 397:176-180
#title Genomic sequence comparison of two unrelated isolates
human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
#accession B71811 #variety #accession #cross-references MUID:96042508 #\*residues 1-220 ##label ARN
##cross-references GB:AE001562; G
##experimental\_source strain J99 ##molecule\_type DNA \*\*status preliminary; translated from GB/EMBL/DDBJ
##molecule\_type mRNA
##rosid...-##status 83 AVFLSKLFGLDY 94 1 ASYLSTSFSLDY 12 3 YLSTSFSLDY 12 3 YLDSSYKMDY 12 14 13 E64708 #type complete
conserved hypothetical integral membrane protein HP1509
Helicobacter pylori (strain 26695)
#formal\_name Helicobacter pylori
09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change jhp1402
#superfamily Escherichia coli ygiH protein
#length 220 #molecular-weight 23804 #che 167437 Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Tilly, J.L. Endocrinology (1995) 136:5042-5053
Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cells of the ovarian follicle. strain J99 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change #formal\_name Helicobacter pylori A71800 hypothetical protein jhp1402 - Helicobacter pylori (strain J99) Conservative Conservative lm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brov Dolg, P.C.; Smith, D.R.; Noonan, B.; Gulld, B.C.; C B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; G.F.; Trust, T.J. 05-Mar-1999 preliminary 65.9%; 50.0%; #type complete Score 54; DB 2; Pred. No. 1.53e+01 2; Mismatches Score 54; DB 2; L Pred. No. 1.53e+01; 3; Mismatches 2 GB:AE001439; Length 220; NID:g4156017; PID:g4156023 ω --2 Length 212; Indels Indels #checksum 0 0 9738 Brown, E.D.; Gaps Gaps deJonge, R.; Vovis, 0 0,

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ACCESSIONS
REFERENCE
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                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #Journal Biochem. Biophys. Res. Commun. (1997) 231:770-774

#title Specific expression of CPP32 in sensory neurons of mouse embryos and activation of CPP32 in the apoptosis induced a withdrawal of NGF.

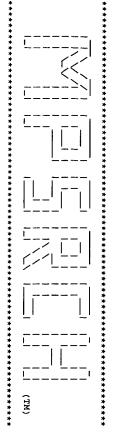
#cross-references MUID:97224429

#accession JC5410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
##cesidues 1-262 ##label TOM
##cross-references GB:AE000649; GB:AE000511; NID:g2314687; PID:g2314690;
##cross-references GB:AE000649; GB:AE000511; NID:g2314687; PID:g2314690;
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                                                                                                                                                                                                                                                                                                                                                 This protein is involved in the apoptosis of dorsal root ganglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references DDBJ:D86352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
                                                                 32 YLDSSYKMDY 41
                                                                                                                                       Local Similarity
les 5; Conser
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llarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                           #length 277 #molecular-weight 31392 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Mus musculus #common_name house mouse
10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change
17-Mar-1999
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translation not shown
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in - mouse
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Pred. No. 1.53e+01;
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Search completed: Thu Sep Job time: 15 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:40:39 1999; MasPar time 1.39 Seconds 87.779 Million cell updates/sec

Title: >US-08-599-226-31
Description: (1-12) from USO8599226.pep
Perfect Score: 82

Scoring table: PAM 150
Gap 15

Sequence:

1 ASYLSTSFSLDY 12

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Statistics: Mean 16.747; Variance 61.471; scale 0.272

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description		Pred. No.
_		5	277	2	us-08-890-	Sequence 2,	Applicatio	
2	52	63.4	306	ω	T-US	Ф	Applica	9.53e+01
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7		9	960	Ν		Sequence 8,	licati	٠.
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12		8	329	<u>س</u>	US-08-348-	Sequence 12	, Applicati	Ŀ
13			343	سر	US-08-348-	æ	, Appl	.18e+0
14			969	<b>ب</b> ـــا	us-07-671-	Sequence 4,	Applicatio	.18e+0
15		ω.	1174	ω	PCT-US95-0	e 2	, Applicati	•
16		8	1174	N	US-08-639-	е 2	, Applicati	L
17		8	1174	<b>_</b>		e 2	, Applicati	2.18e+02
18		8	1174	_	US-08-239-	N	, Applicati	Ŀ
19		8	1174	N	US-08-598-	e 2	, Applicati	2.18e+02
20		æ	1177	4	5169629-2		5169629.	
21		æ	1177	_	US-07-828-	Sequence 8,	Applicatio	
22		00	1177	w	PCT-US92-1	Sequence 8,	Applicatio	2.18e+02
23		80	1177	_	US-07-920-	Sequence 2,	Applicatio	

44	43	42	41	40	39	38	37	36	35	34	33	32	<u>3</u> 1	30	29	28	27	26	25	24
47	47	47	47	47	47	47	47	47	47	47	47	47	48	48	48	48	48	48	48	48
57.3 57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	58.5	58.5	58.5	58.5	58.5	58.5	58.5	58.5
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PCT-US95-0 US-08-760-	US-08-464-	US-08-068-	US-08-464-	us-08-068-	5320941-2	PCT-US93-0	US-08-118-	US-08-810-	PCT-US95-0	US-08-531-	US-08-447-	US-08-447-	US-08-639-	US-08-239-	PCT-US95-0	US-08-349-	US-08-598-	US-08-463-	US-08-446-	5254799-5
Sequence 2, Applicatio Sequence 2, Applicatio	ω `	ω	Sequence 1, Applicatio	Sequence 1, Applicatio	Patent No. 5320941.	Sequence 52, Applicati	52,		Sequence 5, Applicatio	Sequence 29, Applicati	Sequence 7, Applicatio	Sequence 8, Applicatio	Sequence 34, Applicati	•	Sequence 34, Applicati	Sequence 34, Applicati	34,	Sequence 5, Applicatio	Sequence 5, Applicatio	Patent No. 5254799.
2.67e+02 2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.67e+02	2.18e+02	2.18e+02	2.18e+02	2.18e+02			2.18e+02	2.18e+02

## ALIGNMENTS

8888888888888	3888888888888	£88888888888	RESULT ID U XX AC x XX DT DT XX S DE S S
ATTORNEY/AGENT INFORMATION:  NAME: Gaylo, Paul J.  REGISTRATION NUMBER: 36,808 REFERENCE/DOCKET NUMBER: x-10704 TELECOMMUNICATION INFORMATION: TELEPHONE: (317) 276-0756 TELEFAX: (317) 276-3861 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 277 amino acids TYPE: mino acids	olis olis olis form: for	Sequence 2, Application US/08890542A Patent No. 5840509 GENERAL INFORMATION: APPLICANT: Ni, Binhui APPLICANT: Ni, Binhui APPLICANT: Wu, Xin TITLE OF INVENTION: PROTEASE AND RELATED NUCLEIC ACID TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSE: Eli Lilly and Company STREET: Lilly Corporate Center	US-08-890-542A-2 STANDARD; PRT; 277 AA.  XXXXXX  Sequence 2, Application US/08890542A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application PC/TUS9506119 GENERAL INFORMATION:
                                              67
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: AMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 YLDSSYKMDY 41
                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
QUENCE 306 AA: 33942 MW; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.DOS/MS-DOS/ASCII
SOTTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 16-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, V
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                             YFDSTFELEY 76
                           YLSTSFSLDY 12
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CONCUCLASSIFICATION:
                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston
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larity 40.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                             UMBER: PCT/US95/06119
CONCURRENTLY HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                 Score 52; DB 3; Le
Pred. No. 9.53e+01;
4; Mismatches 2;
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                                                                                                           497482 CN;
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                                                                                      Length 306;
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                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                               Patent No.
                                                                                                                          APPLICANT: Zupancic, Thomas APPLICANT: Shafer, Alan W TITLE OF INVENTION: Hu-B1 TITLE OF INVENTION: RECEPTION OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                               67 PSYLTGEFPGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Anti-sen
TITLE OF INVENTION: Chloroph
NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,929
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 267 AA; 28387 MW; 353655 CN;
                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                           APPLICANT: Snodgrass, H. I
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thoma
APPLICANT: Shafer, Alan W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 267 amino acids
                                                        COUNTRY: USA
ZIP: 10036-2711
                                                                                      CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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17. 5869610
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                                                                          New York
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                                                                                               E: Pennie & 1155 Avenue
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    FastSEQ for Windows Version
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                                                                                                                                         RECEPTOR
                                                                                                                                                Alan W.
Hu-B1.219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-sense RNA for CAB
Chlorophyll Content in
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Pred. No. 1.78e+02;
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-588-526-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXX
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08588526
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                                                                                                                                                                                                                                                                                                                                                  Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                             APPLICANT: Zupancic, Thom APPLICANT: Shafer, Alan TITLE OF INVENTION: DETECTIVE OF INVENTION: VARIATIVE OF INVENTION: AND MUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YLSTSFSLDY 12
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MOLECULE TYPE:
FRAGMENT TYPE:
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APPLICANT:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION UMBER: US/08/588,526
FILING DATE: 18-DAN-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                           STREET: 1155 AV CITY: New York STATE: New York COUNTRY: US
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TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SE TYPE: protein NT TYPE: internal 898 AA; 102731 MW;
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10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                          New York
                                                                                                                                                                                                            E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                      Cioffi, Joseph
Zupancic, Thomas
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05-AUG-1996
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Pred. No. 1.78e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/08693697
                                                                                                                                                                                                                COUNTRY: USA
ZIP: 1036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                 TELEFAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acid
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                                    "YPE: amino acids
STRANDEDNESS: sir
TOPOLOGY: 1'
YAL"
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REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHAX: 650-493-5556
TELEPAX: 650-493-5556
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MOLECULE TYPE: protein
UENCE 908 AA; 103856 MW; 4758599 CN;
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
                                FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                      STATE: New York
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                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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o. 5869610
                     LE TYPE: protein
NT TYPE: internal
908 AA; 103702 MW; 4753903 CN;
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 59.8%; Score 49;
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Pred. No. 1.78e+02;
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Length 908;
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                       US-08-588-190-3
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                                                                                       Local Similarity
                                                                19 YVITAFNLSY 28
                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
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TELEFAX: 650-493-5556
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FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1 219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
                                                                                                                     MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                    YLSTSFSLDY
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                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
DLECULE TYPE: pro
                                                                                                                                                                                            NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New Yor
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                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                             SE TYPE: protein 960 AA; 109634 MW; 5296019 CN;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                        New York
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                 USA
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Cioffi, Joseph
Zupancic, Thomas J.
                                                                                       59.8%;
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                       STANDARD;
                                                                               Score 49; DB 2; I
Pred. No. 1.78e+02;
3; Mismatches 2
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Query Match
Best Local Similarity
Matches 5; Consei
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                                                                                                   Sequence 8, Application US/08355888A
                                                                                                                                                                                                        US-08-355-888A-8
Sequence 8, Application US/08355888A Patent NO. 5763211
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08588190 Patent No. 5856098
                                                                                                                                                                                                                                                                                                        19 YVITAFNLSY 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: IIIII
MOLECULE TYPE:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                         3 YLSTSFSLDY 12
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APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
TITLE OF INVENTION: VARIANT AND METHODS FOR REGULATING OBESITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18-JAN-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
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SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino STRANDEDNESS:
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larity 50.0%;
Conservative
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109698 MW; 5295408
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Pred. No. 1.78e+02;
3; Mismatches 2
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Best Local 9
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                                                                                                                                                            Sequence 5, Application PC/TUS9608730
                                                                                                                                  Sequence 5, Application PC/TUS9608730 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
EQUENCE 960 AA: 109634 MW; 5296019 CN;
                                                                                                                                                                                                                                                                                                                                                                        NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                              19 YVITAFNLSY 28
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                               3 YLSTSFSLDY 12
                                                                               APPLICANT: Cassels, Frederick
APPLICANT: Anderson, Jeffrey
APPLICANT: Carter, John Mark
TITLE OF INVENTION: Methods of Raising Antibodies Against E.
TITLE OF INVENTION: Coli of the Family CSF-CFA./1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Glenna Hendricks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zupancic, Thomas J. APPLICANT: Shafer, Alan W. TITLE OF INVENTION: Hu-Bl.219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 14-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                           COUNTRY: USA
ZIP: 22031
                                                  STREET: P.O. 1
CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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10036-2711
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                                                            P.O. Box 2509
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                                                                                                                                                                                                              STANDARD;
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Pred. No. 1.78e+02;
3; Mismatches 2;
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Query Match
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Local Similarity 50.0%;
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ATTORNEY AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: PCT/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 591-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASYLSTSFSLDY 12
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cassels, Frederick
APPLICANT: Anderson, Jeffrey
APPLICANT: Carter, John Mark
TITLE OF INVENTION: Methods of Raising Antibodies Against
TITLE OF INVENTION: Coli of the Family CSF-CFA./1
                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08730
FILING DATE: 03-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 591-4470
                                                                                                                                                                                                                                                               ZIP: 22031
COMPUTER READABLE FORM:
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APPLICATION NUMBER: PC
FILING DATE: 03-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Hendricks, Glenna
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                           STREET: P.O. I
CITY: Fairfax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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(703) TD NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                Glenna Hendricks
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Pred. No. 2.18e+02;
3; Mismatches
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                                       PCT/US96/08730
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TELEFAX: (703) 591-4428 INFORMATION FOR SEQ ID NO: 11:

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Best Local S
Matches
Query Match
                                                    TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5576423
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL GREGORIO
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Viles, Jan E.
APPLICANT: de Viles, Jan E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12,
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nes 6; Conservative
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                                                                                                              ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION UMBER: 34,090

REFERENCE/DOCKET NUMBER: DX04

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-652-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: internal QUENCE 117 AA; 12389 MW; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>,,,</u>
                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 03-DEC-1994
CLASSIFICATION: 530
CLASSIFICATION: 530
               TOPOLOGY: linear
MOLECULE TYPE: protein
MENCE 329 AA; 36590 MW; 607424 CN;
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASYLSTSFSLDY
                                                                                                                                                                                                                                                                                                                ADDRESSEE: DNAX Res
STREET: 901 Califor
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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                                                                   329 amino acids
                                                                                                                                                                                                                                                                                                                                       E: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                         USA
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50.0%;
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 Score 48;
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Pred. No. 2.18e+02;
3; Mismatches 3;
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DB 1;
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                                     US-07-671-817A-4
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INFORMATION FOR SEQ ID NO:
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3 YLSTSFSLDY
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                                                                                                                                                         MOLECULE TYPE: protein JENCE 343 AA; 38094 MW; 663822 CN;
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NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 03-DEC-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acid
                                                                                                                                                                                                                                         TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 901 Cal
CITY: Palo Alto
STATE: Californ
                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                                                TOPOLOGY:
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Pred. No. 2.18e+02;
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                                                                                                            Sequence 29, Application PC/TUS9505431
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                                                                                                                                                                                                                                    653 TYLSDEFCLD 662
                                                                                         Sequence 29,
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SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4,
                                                                               Sequence 29, Application GENERAL INFORMATION:
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          APPLICANT:
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MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: protein
JENCE 969 AA; 109598 MW; 4754786 CN;
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APPLICATION NUMBER: GB 8823068.5
FILING DATE: 30-SEP-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICANT: Ely, Susan
APPLICANT: Tippett, Janet M
TITLE OF INVENTION: DNA constructs
NUMBER OF SEQUENCES: 6
                                                            APPLICANT:
                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 861-3000
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 APPLICANT:
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FILING DATE: 29-SEP-1989
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City: San Diego
State/Province:
Phone number:
Telex number:
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          (619) 453-8030
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                                                                    646 TYLSDEFCLD 655
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TELEFAX: (904) 372-58
INFORMATION FOR SEQ ID NO:
                                             2 SYLSTSFSLD 11
                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1174 AA; 133119 MW; 7052059 CN;
                                                                                                                                                                                                                                                                                           NAME: Saliwanchik, David
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com.
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MA83 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Importance of INVENTION: Pse NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/05431
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                      Similarity
                                                                                            Conservative
                                                                                                                                                                                                                      : (904)
(904) 372-5800
(906) TD NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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          2 12:40:46 1999
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Pred. No. 2.18e+02;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:41:55 1999; MasPar time 3.46 Seconds 73.821 Million cell updates/sec

Title: >US-08-599-226-32\_\_\_\_\_\_ Description: (1-12) from US08599226.pep Perfect Score: 78 Sequence: 1 ASYLSTSSSLHY 12

Scoring table: PAM 150 Gap 15

earched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.195; Variance 56.541; scale 0.304

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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78 69 60 60 60 60 60 60 60 60 60 60 60 60 60	Score
100 888.5 88.5 88.5 80.8 80.8 73.2 73.1 73.1 73.1 73.1 73.1 73.1 73.1 73.1	Query Match
12 27 12 27 12 27 12 27 121 27 121 27 12 27 22 27 23 23 321 23 321 23	Length DB
W27591 W27598 W27593 W27593 W27593 W27589 W27589 W27589 W27589 W27589 W27589 W27594 W27563	3 ID
Anti-TWF-alpha antibo Banka gouldi endoglu Anti-TWF-alpha antibo	Description
1.96e+00 1.85e+00 6.27e+00 6.27e+00 7.99e+01 3.3e+01 3.3e+01 1.36e+02 1.33e+02 1.33e+02 1.33e+02 1.33e+02 1.33e+02 1.33e+02 1.33e+02 1.33e+02 1.33e+02 1.67e+02	Pred. No.

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Human tumour suppress Extracellular portion	Sequence of c-erbB-2	rotein.	plasmic	Her2-GM-CSF immunosti	beta-3	adrena	Canine beta-3 adrener	Bovine beta3 adrenerg	adren	ne beta-	drener	renergic	-pr	G-protein coupled hum	ErbB2 protein	ErbB2 doma	te-	sequence of	ence of	٠	H. pylori ORF 09cp107	קַ	:	H. pylori ORF 06cp306	×	đ	Arabidopsis p-hydroxy
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The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmo resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylltis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
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Matches 1
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WPI; 97-415302/38.
High affinity antibodies ag
TNF alpha activity, e.g. to
Claim 20; Page 73; 102pp; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary discorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                      endothelial
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tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3
tumour necrosis factor-alpha; TNF-alpha; inhibition;
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                   (HUVEC).
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Pred. No. 1.96e-01;
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Query Match Best Local

Local Similarity

98 91

Score Pred.

No.

DB 27; 1.85e+00;

Length

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     Z E P A E
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                                                                                                                                                                                                                                                                                                                                    The present sequence is a novel anti-human tumour necrosis

C factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity

C determining region 3 (CDR3).

C The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

C less and has a Koff rate constant of 1x10 power -3 s power -1 or

Cless and has a Koff rate constant of 1x10 power -3 s power -1 or

C less (both determined by surface plasmon resonance), and

C neutralises human TNF-alpha cytotoxicity in a standard in vitro

C 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

C 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

C autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

S condylitis, osteoarthritis, gouty arthritis, rheumatoid

spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

C syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal

CC ardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

Ab also inhibits TNF-alpha induced expression of endothelial cell
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                     Query Match
Best Local :
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disease; autoimmune disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; EHAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3
                                                      W27592 standard; peptide; 12 W27592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salfeld JG, Schoer WPI; 97-415302/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W27593 standard;
W27593;
                    Anti-TNF-alpha antibody
                                                                                                                                                                                                                                                                                                            endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                       L9-MAR-1998
                                                                                                                                                                                                                                                                                                          leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein andothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0-FEB-1997;
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                                                                                                                                                                                                                                      Similarity
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                                   (first entry)
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               heavy chain CDR3.
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Pred.
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                                                                                                                                                                                                                                     DB 27;
3.03e+00;
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                                                                                                                                                                                                                                                    Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer
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Allen DJ, Hogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
WPI; 97-415302/J8.

High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
TR alpha activity, e.g. to treat autoimmune diseases and cancer
SC Claim 20; Page 74; 102pp; English.

The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
C determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less (both determined by surface plasmon resonance), and
c neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an ICSO of 1x10 power -7 M or less. The Ab, which
inhibits TNF-alpha activity, can be used to treat sepsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein scarcing and the star of the s
                                                                                                                                                                                                                                      malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                 keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                           Anti-TNF-alpha antibody heavy chain variable region.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
heavy chain; variable region; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W27569 standard; Protein; 121 AA. W27569;
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25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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                                                            W09729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malignancy; pulmonary disorder; intestinal disorder; hepat
cardiac disorder; inflammatory bone disorder; reperfusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human umbilical vein endothelial cell.
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                                                                                                                        human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             l9-MAR-1998 (first entry)
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 27; Le
Pred. No. 6.27e+00;
1; Mismatches 1;
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erfusion injury;
burn; ELAM-1;
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CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain variable region. CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Koff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmon resonance), and contralises human TNF-alpha cytotoxicity in a standard in vitro CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which CC inhibits TNF-alpha activity, can be used to treat sepsis. CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, cardiactor, viral or fulminant hepatitis, coagulation disturbances, human correficion injury when it has a correficion injury when it is a correstion.
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                                                                                                                                                                                                      14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
                                                    Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.

High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; page 74; 102pp; English.
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Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky b,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                     Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton
                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                        keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  burns, reperfusion injury, keloid formation, scar tissue formatio pyrexia, periodontal disease, obesity and radiation toxicity. The hb also inhibits TNF-alpha induced expression of endothelial cell
               The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain compleme
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09-FEB-1996; US-599226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukocyte adhesion molecule-1 (ELAM-1) on human umbilical
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Pred. No. 7.99e+00
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        HUVEC;
                 complementarity
                                                                              cancer
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                                                                                                  to inhibit
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Best Local
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The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, allocholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or cless (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1p29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diseases, alignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell
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25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; benefusion disease; coagulation disturbance; burn; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical relation toxicity; human umbilical relations distablish and complete the second contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W27586 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endothelial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BADI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukocyte adhesion molecule-1 (ELAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.2%;
larity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-031476.
US-599226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endothelial cell.
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Pred.
0; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               re 61; DB 27; Le
d. No. 1.29e+01;
Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on human umbilical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infectious disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                       to inhibit
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Matches

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                                                                                                                         The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNR-alpha) antibody (Ab) heavy chain complementarity
determining region 3 (CDR3).
The Ab dissociates from TNF-alpha with a Kd of ix10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
less (both determined by surface plasmon resonance), and
inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
salcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
Ab also inhibits TNF-alpha induced expression of endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Salfeld JG, Schoenhaur D, Salfeld Seases and TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 73; 102pp; English.

Claim 20; Page 73; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1997.
10-FEB-1997;
25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BADI ) BASF AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan 2, Labkovsky
Ankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Mankovich JG, Schoenhaut D, Vaughan TJ, White M, Wilto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mallgnancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy chain; complementarity determining region 3; inhibiti treatment; sepsis; disease; autoimmune disease; infectious
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W27589 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
                                                                             Sequence
                                                                                                 endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-TNF-alpha antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endothelial cells
                                                                                                                 eukocyte adhesion molecule-1 (ELAM-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tocal Similarity 100.0%; hes 10: Constitution 10.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASYLSTSSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
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NF-alpha antibody heavy chain CDR3.
NF-alpha; antibody; CDR3.
tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3
tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3
                   h 73.
Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 AA;
                                                                             12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; U02219.
; US-031476.
; US-599226.
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                                                                                             (HUVEC).
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                   . 18;
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Score
Pred.
0; M
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Pred.
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                   57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57; DB 27;
No. 3.33e+01;
                 ; DB 27;
. 3.33e+01;
                                                                                                                 ဓ္ဌ
                                                                                                                 human
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                                   Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer
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RESULT
ID W
AC W
DT 2
DE B
KW E
KW C
KW C
FD OS B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determining region 3 (CDM3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diseases, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone recorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, puravia pariodoral disease obscitus and redicates toxicity men
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
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W09729131-A1.

14-AUG-1997.

10-FEB-1997; U02219.

25-NOV-1996; US-033476.

09-FEB-1996; US-599226.

(BADI ) BASF AG.
                           Bankia gouldi endoglucanase.

Bankia gouldi endoglucanase.

Endoglucanase; cellulase; carboxymethylcellulose; cellulose;

blomass; beta-1,4-glycosidic bond; hydrolysis; saccharificat
thermostable enzyme; thermophilic; glycosidase.

Bankia gouldi mix (Clone 37GP2).
                                                                                                                                                                                  LT 10
W34987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-TNF-alpha antibody heavy chain CDR3.

Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

heavy chain; complementarity determining region 3; inhibition;

treatment; sepsis; disease; autoimmune disease; infectious disease;

malignancy; pulmonary disorder; intestinal disorder; hepatitis;

cardiac disorder; inflammatory bone disorder; reperfusion injury;

bone resorption disease; coagulation disturbance; burn; ELAM-1;

beniodontal disease; obesity; radiation toxicity;

periodontal disease; obesity; radiation toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.

WPI; 97-415302/38.

High affinity antibodies against human TNF alpha - useful to inh: TNF alpha activity, e.g. to treat autoimmune diseases and cancer Claim 20; Page 73; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
  thermostable enzyme; ther
Bankia gouldi mix (Clone
WO9744361-A1.
27-NOV-1997.
                                                                                                                                                               W34987;
                                                                                                                                                                                                                                                                                                                                                                                                                         endothelial cells (HUVEC).
Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endothelial cell
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W27587 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                 1 asylstsssl 10
                                                                                                                                                                                                                                                                  ASYLSTSSSL 10
                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukocyte adhesion molecule-1;
vein endothelial cell.
                                                                                                                                                                                Protein;
                                                                                                                                                                                  875
                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 27;
Pred. No. 3.33e+01;
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                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                 Length 12;
                                                                               saccharification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                      14 AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1997; U08793.
22-MAY-1996; US-651572.
(RECO-), RECOMBINANT BIOC
Lam DE, Mathur EJ;
WPI; 98-018435/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endoglucanase(s), preferably form archael bacterium, AEPII lauseful to degrade carboxymethylcellulose and hydrolyse of beta-1,4-glycosidic bonds in cellulose Claim 1; Fig IC: 164pp; English.

This protein comprises an endoglucanase of Bankia gouldi mix (clone 37GP2) that is capable of degrading carboxymethylcellulose and of hydrolysing the beta-1,4-glycosidic bonds in cellulose. It has homology to an endoglucanase of archaebacterium AEPIIIa (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w27594 standard; peptide;
w27594;
19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology to an endoglucanase of archaebacterium AEPIIIa (see W34985). It can be produced from native cells or from recombinant host cells, especially prokaryotic host cells transformed with a plasmid or virus-derived vector including the endoglucanase DNA (see T94195). 24 Endoglucanases (see W34986-W35008) are claimed. They can be used to degrade cellulose for the conversion of plant biomass into fuels and chemicals, for use in detergents, textiles, animal feed, waste treatment, and in the fruit juice and brewing industries for the clarification and extraction of juices. Sequence 875 AA;
                                                                                                                                                                                                                                Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                      keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukoyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                            WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                    (BADI )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASYLSTSSSLHY
                                                                                                                                                                                                                                                                                  BASF AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 28;
Pred. No. 1.06e+02;
2; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                       HUVEC ;
                                                                                                                                              complementarity
                                                                                                   power -1 or
            multiple
                                                                      in vitro
                                                                                                                                                                                           to inhibit
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                                          PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer PS Claim 9; Page 65; 102pp; English.

CT he present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CDR3).

CT he Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro class (both determined by surface plasmon resonance), and cultivity, can be used to treat sepsis, and this is the standard in vitro class and has a civity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylltis, osteoarthritis, gouty arthritis, rheumatoid spondylltis, osteoarthritis, gouty arthritis, allergy, multiple csclerosis, autoimmune diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, calcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell vein
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-1997;
25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38
High affinity antibodies against human TNF alpha - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepartitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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Human; tumour necrosis factor-alpha; TNF-alpha;
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                  endothelial
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                                    leukocyte adhesion molecule-1 (ELAM-1) on
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: US-599226.
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Pred. No. 1.33e+02;
Mismatches 0;
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Best Local :
Matches
                                                                         S Claim 8; Page 63-64; 96pp; English.

(Novel rat spermatid chemoreceptors D-2, D-7, D-8, D-9 and G-X (W21662-66) represent a new family of putative chemosensory receptors that show homology to, but are different from, receptors deduced from isolated DNA fragments (T72287-91) isolated from rat genomic DNA. Recombinant receptor polypeptides can be produced in host cells for use as immunocontraceptives e.g. in vaccines, to detect specific antibodies which are indicative of autoimmune infertility of an animal by stimulating or inhibiting the binding of ligands to the receptors. Host cells can also be used as vaccines.
                                                Query Match
Best Local
                                      Matches
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08-NOV-1996; U18002.
09-NOV-1995; US-556186.
(UYJO ) UNIV JOHNS HOPKII
Ronnett GV, Ruat M, Sn.
WPI; 97-281033/25.
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W21664;
W21664;
29-SEP-1997
                                                                                                                                                                                                        autoimmune infertility
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larity 88.9%;
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/note= "transmembrane
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Snyder SH,
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  p-hydroxyphenylpyruvate dioxygenase p-hydroxyphenylpyruvate dioxygenase; inhibitor tolerance; overexpression; herbicide.
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15-MAY-1997.
08-NOV-1996; U18002.
09-NOV-1995; US-556186.
(0YJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Ronnett GV, Ruat M, Snyder SH, Walensky L;
WPI; 97-281033/25.
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W21665;
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W41941 standard;
W41941;
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Sperm receptor;
infertility.
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/note= "transmembrane
279..298
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/note= "transmembrane
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203..2
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/note= "transmembrane
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Pred. No. 1.33e+02;
3; Mismatches 2;
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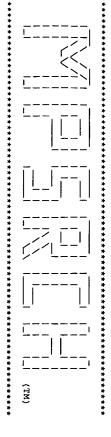
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Search completed: Thu Job time: 20 secs.
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                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                Plant p-hydroxy:phenyl:pyruvate dioxygenase enzyme - used to isolat compounds that inhibit the p-hydroxyphenylpyruvate dioxygenase rate of reaction for use as herbicides. Claim 4; Pages 49-51; 72pp; English.
The present sequence is Arabidopsis thaliana truncated p-hydroxyphenylpyruvate dioxygenase (p-HD). The p-HD cDNA can be used to impart tolerance to a compound that inhibits the rate of reaction of p-HD, or to overexpress p-HD. A compound that inhibits the activity of p-HD can be used as a herbicide.

Sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                      (DUPO ) DU PONT DE NEMOURS & CO E I. Gutterldge S, Maxwell CA, Scolnik PA, WPI; 98-077179/07.
N-PSDB; V04491.
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31-DEC-1997.
36-JUN-1997; U11295.
27-JUN-1996; US-021364.
                                                                                      58 asylltsgdlrf
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                                                             ASYLSTSSSLHY
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                                                                                                                       64.1%;
larity 58.3%;
Conservative
               Sep
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                                                                                                                                      Score 50; DB 29;
Pred. No. 1.67e+02;
                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Wittenbach VA;
                                                                                                                                                    Length 417
                                                                                                                       Indels

    used to isolate
dioxygenase rate

                                                                                                                       0
                                                                                                                       Gaps
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:44:21 1999; MasPar time 1.37 Seconds 88.617 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Title: >US-08-599-226-32 (1-12) from US08599226.pep 78

Sequence: 1 ASYLSTSSSLHY 12

Scoring table: PAM 150 Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued
1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 16.037; Variance 54.698; scale 0.293

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

esult No.	Score	Query Match	Length DB	₩	ID	Description		Pred. No.
н	49		400	2	US-08-103-	Sequence 9,	Applicatio	9.84e+01
N	49	62.8		_	-08-46		licat	
ω	49		491	_	-08-17		Applicatio	
4	48			_	us-08-066-	Sequence 59	•	
<sub>5</sub>	48			N	US-08-828-	Sequence 3,	Applicatio	1.23e+02
σ	48			N	US-08-828-	Sequence 1,	Applicatio	1.23e+02
7	48			w	PCT-US93-0	Sequence 16	•	1.23e+02
8	48			_	US-08-118-	Sequence 16	•	1.23e+02
9	48			_	US-08-087-	Sequence 2,	Applicatio	1.23e+02
10	48			_	US-07-916-	Sequence 6,	Applicatio	1.23e+02
11	48			۳	US-08-351-	Sequence 4,	Applicatio	1.23e+02
12	48			ш	US-08-351-	Sequence 5,	Applicatio	1.23e+02
13	48			μ.	US-07-783-	Sequence 1,	Applicatio	1.23e+02
14	48			<b></b> 4	US-08-444-	Sequence 6,	Applicatio	1.23e+02
15	48			سا	US-08-087-	Sequence 15	, Applicati	1.23e+02
16	48			μ,	US-08-351-	Sequence 2,	Applicatio	1.23e+02
17	48			1	US-07-916-	Sequence 2,	Applicatio	1.23e+02
18	48			_	US-08-351-	Sequence 3,	Applicatio	1.23e+02
19	48			N	US-08-386-	Sequence 2,	Applicatio	1.23e+02
20	48			N	US-08-414-	Sequence 68	•	1.23e+02
21	48			2	US-08-625-	Sequence 2,	Applicatio	1.23e+02
22	48		1255	۳	US-08-467-	Sequence 68	•	1.23e+02
23	48			N	US-08-468-		•	1.23e+02

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25
46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	47	47	48	48
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US-08-785-	US-08-922-	US-08-936-	us-08-936-	US-08-936-	US-08-714-	US-08-630-	US-08-714-	US-08-439-	US-08-439-	US-08-439-	US-08-439-	US-08-439-	PCT-US94-1	PCT-US94-1	PCT-US94-1	PCT-US94-1	PCT-US96-0	PCT-US96-0	US-08-356-	US-08-484-
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Η	Applicatio	Applicati	Applicatio	Applicatio	Applicatio
1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.91e+02	1.53e+02	1.53e+02	1.23e+02	1.23e+02

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9: 010	NAME: Lavalleye, Jean Paul REGISTRATION NUMBER: 31,451 REFERENCE/DOCKET NUMBER: 2363-017-55	ATTORNEY/AGENT INFORMATION:	APPLICATION NUMBER: US 07/633,060	_	-	APPLICATION NUMBER: US/08/103,170	SOFTWARE: Patentin Release #1.0, Version #1.25	SYSTEM: PC-DOS/MS-DOS	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	COMPUTER READABLE FORM:	2	STATE: Virginia COUNTRY: U.S.A.	Arlington	7	ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.	CE ADDRESS:	SEQUENCES: 41	OF INVENTION: Histomine hi, hz, and his neceptors, methods not	lones Encoding	Gantz, Ira	APPLICANT: Yamada, Tadataka	GENERAL THORMATION:		Sequence 9, Application US/08103170			XXXXXX	LT 1 US-08-103-170-9 STANDARD; PRT; 400 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08462733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 YLAVTNTLRY 143
           453 AGFLTIGADLHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5610019
GENERAL INFORMATION:
APPLICANT: Day, J.
APPLICANT: Albers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2,
                                                                                                                                         TELEPHONE: 206-547-808
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO:
                               Local Similarity 33.3%
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 62.8%;
Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YLSTSSSLHY 12
                                                                        TOPOLOGY: 1i
MOLECULE TYPE:
UENCE 491 AA;
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:

NAME: PAIKET, GATY E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-11D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 26-547-8080 ext 322
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Day, Joseph R.
APPLICANT: Albers, John J.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Adolphson, Janet L.
TITLE OF INVENTION: Phospholipid Transfer Proteins
NUMBER OF SEQUENCE: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             STREET: 422
CITY: Seatt
STATE: WA
COUNTRY: US
ZIP: 98105
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                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens CE 400 AA; 42804 MW;
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                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                   491 amino acids
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4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                         USA
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            464
                                                                         protein
54569 MW;
                                          62.8%;
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                              Score 49; DB 1; Ler
Pred. No. 9.84e+01;
6; Mismatches 2;
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Pred. No. 9.84e+01;
5; Mismatches 1
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Best Local Similarity 33.3%;
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                                    Sequence 59, Application US/08066325
                                                                               XXXXX
                                                                                                   US-08-066-325-59
                                                                                                                                                                                                                                                              TELEPHONE: 206-547-8080
TELEPAX: 205-548-2329
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08176402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
         Sequence 59, Application Patent No. 5667967
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Patent No.
                                                                                                                                                              453 AGFLTIGADLHF 464
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 491 AA; 54569 MW; 1262097 CN;
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 93-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext
TELEPAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Day, Joseph R.
APPLICANT: Albers, John J.
APPLICANT: Lofton-Day, Catherine
APPLICANT: Adolphson, Janet L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Adolphson, Janet L.
TITLE OF INVENTION: Phospholipid Transfer Proteins
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FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 98105
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562
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5622843
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4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                491 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Pred. No. 9.84e+01;
6; Mismatches 2;
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                                                                                                                                                                                                     Length 491;
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Matches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                            US-08-828-832-3
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                       XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                           Sequence 3, Application US/08828832 Patent No. 5827711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/066,325

FILING DATE: 21-MAY-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5667967tenburg Ph.D., Carol

REGISTRATION NUMBER: 39,317

REFERENCY/DOCKET NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                            Match 61.5%;
Local Similarity 41.7%;
                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         \mathbf{L}
                                                                                                                                                                                                                                                                                                                                            4 SSFLGYNSPLHF 15
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                         APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL SUCCINATE DEHYDROGENASE SUBUNIT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bernard, Claudé
TITLE OF INVENTION: T-CELL RECEPTOR VARIABLE TRANSCRIPTS AS DISEASE RELATED
NUMBER OF SEQUENCES: 157
                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                 CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
                                                                     STREET: 31/4 FC-
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                           COUNTRY: U
ZIP: 94304
                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                            3, Application US/08828832
                                                                                                                                                                                                                                                                                                                                                                                                            LE TYPE: peptide
29 AA; 3155 MW; 4596 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
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                                                                 CA
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: SEED and BERRY LLP 6300 Columbia Center,
                                                     USA
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                                                                                                 Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                             STANDARD;
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Pred. No. 1.23e+02;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                       Sequence 1, Application US/08828832 Patent No. 5827711
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                 81 AAYLNPCSAMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 61.5%;
Local Similarity 41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 158 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            1 ASYLSTSSSLHY 12
                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                          COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL SUCCINATE DEHYDROGENASE SUBUNIT NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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LIBRARY: GenBa
CLONE: 1575011
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
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           ATTORNEY/AGENT INFORMATION:
                                                  APPLICATION NUMBER: U: FILING DATE: Herewith CLASSIFICATION: 435
                                                                                                                                                                   STREET: 3174 POI
CITY: Palo Alto
STATE: CA
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TOPOLOGY: 11
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REGISTRATION NUMBER:
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                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                    ADDRESSEE: Incyte Pharmace STREET: 3174 Porter Drive
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E: 1575011
158 AA; 17096 MW; 135076 CN;
Billings, Lucy J.
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                                                                                                                           Diskette
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WBER: 36,749
                                                                       US/08/828,832
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Pred. No. 1.23e+02;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application PC/TUS9308528 GENERAL INFORMATION:
                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: TOWNSEND, KEVIN G.

RECISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY-2 POTELEPHONE: 703-678.7107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 AAYLNPCSAMDY 93
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Local Similarity 41.7%;
es 5; Conservative
                                                                INFORMATION FOR SEQ ID NO:
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                              SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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             TOPOLOGY: lir
                                                                                    TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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CLONE: 2454416
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419 Seventh Street, N.W.,
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Pred. No.
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Best Local
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US-08-118-270-16
                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Mulphy, Randall B.
APPLICANT: Schuster, David I.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND MI
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                                                Local Similarity
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INFORMATION FOR SEQ ID NO:
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                                                                              TOPOLOGY: 11:
MOLECULE TYPE:
PUENCE 362 AA;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 10-SEP-J
                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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NAME: Townsend, Kevin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLSTSSSLHY 12
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UP ZIP: 20004
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                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                             NAME: Townsend, Kevin REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 09-SEP-1993
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                                                                                                                       TYPE:
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                                       61.5%;
larity 40.0%;
Conservative
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Street, N.W.,
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38722 MW;
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38722 MW;
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Pred. No.
5; Misma
                                      Score 48; DB 1; 1
Pred. No. 1.23e+02
5; Mismatches
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No. 1.23e+02;
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Best Local Similarity
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    Patent No. 5364772
GENERAL INFORMATION:
APPLICANT: Grannema
APPLICANT: Lahners.
APPLICANT: Rao, Dor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein SEQUENCE 388 AA; 41667 MW; 771830 CN;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino
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                                                                                                                                                                   Sequence 6, Application US/07916901
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                                                                                                     Sequence 6, Application US/07916901 Patent No. 5364772
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Patent No.
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TITLE OF INVENTION: Nucleotide Sequences Encoding
TITLE OF INVENTION: Beta3-Adrenergic Receptor and
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                       10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Linker, Raymond O. REGISTRATION NUMBER: 26, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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    Application US/08087772A
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Granneman, James &
Lahners, Kristine
Rao, Donald D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Emorine, Jean L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%;
                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                  James G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 1; L
Pred. No. 1.23e+02;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3339-195
                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                             400 AA
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Their Applications
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                                                                                                                                                                                                                                       Sequence 4, Application US/08351473B
                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                                                                                                                                                                                                                                                                                       133 YLAVTNPLRY 142
                                                                                                                                                                                                         Sequence 4, Application US/08351473B Patent No. 5656440
                                                                                                                                                                                            Patent No. 5656440 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  3 YLSTSSSLHY 12
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS,MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                APPLICANT: LENZEN, GERLIND APPLICANT: KAPOOR, ARCHANA TITLE OF INVENTION: NUCLEO TITLE OF INVENTION: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY
ADDRESSEE: MILTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CURRENT APPLICATION DATA:
                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (313) 689-3554
                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                   STREET: 1755 S.
CITY: ARLINGTON
STATE: VIRGINIA
                                                               COUNTRY: UZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 19920' CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 201 W. I
CITY: Troy
STATE: Michigan
                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                             4.
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
          PatentIn Release #1.0,
                                                                                                        OBLON, SPIVAK,
55 S. JEFFERSON
                                                                                                                                                                                                                                                                                                                                                                                                     61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19920720
                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                  NUCLEOTIDE SEQUENCES CODING FOR THE BOYINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/07/916,901
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Pred. No. 1.23e+02;
5; Mismatches 1
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                                                                                                       MCLELLAND, MAIER & NEUSTADT DAVIS HIGHWAY, SUITE 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CN;
          Version
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       #1.30
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ATTORNEY_AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-3000
TELEFAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08351473B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08351473B Patent No. 5656440
                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YLSTSSSLHY 12
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 | 1907 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 93 04
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 93 04670
                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON
STREET: 1755 S.
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                           APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
                                                                                                                                                                                                                                                                                      ZIP:
                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/351,473B FILING DATE: 21-FEB-1995
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55 S. JEFFERSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT/FR94/00447
                       PCT/FR94/00447
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Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 400 AA; 43005 MW; 820814 CN;
                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/077836020 Patent No. 5418160
                                                                                                                       REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YLSTSSSLHY 12
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Polypeptide
JENCE 400 AA; 43166 MW; 843002 CN;
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01
FILING DATE: 19911101
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: J.G. Mullins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 66
                                                                                     TYPE: AMINO ACID
                                                                                                                                                                                                                      REGISTRATION NUMBER: 33073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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E: Virginia
TRY: USA
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Suite 300,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Craig Venter et al PENTION: A FAT CELL SPECIFIC a-ADRENERGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Price, LeBlanc & Becker
0, 99 Canal Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR
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Pred. No. 1.23e+(
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Length 400;

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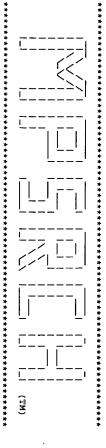
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Best Local Similarity
Matches 4; Conser
Query Match
                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-444-734A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                       NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH065.001FW1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-9404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/444,734A FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,917
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/548,714
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                        LENGTH: 402 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                               TOPOLOGY:
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                     VT TYPE: internal 402 AA; 42931 MW; 794255 CN;
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larity 40.0%;
Conservative
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Mahan, Lawrence
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                                                                               linear
61.5%; Score 48; DB 1;
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Lawrence C.
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Pred. No. 1.23e+02;
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Search completed: Thu Sep Job time: 7 secs.
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                                                                                                    Matches
                                                                                                                              Query Match
                                                                                                                   Best
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NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                         SEQUENCE
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                                                                           136 YLAVTNPLRY 145
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GENERAL INFORMATION:
                                                                                                                 / Match 61.5%;
Local Similarity 40.0%;
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APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
APPLICANT: Emorine Murine
APPLICANT: Nucleotide Sequences Encoding the Murine
APPLICANT: Nahmias, Jean L.
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 402 AA; 42931 MW; 794255 CN;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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LENGTH: 402 amino acid
                                                   YLSTSSSLHY 12
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ZIP: 28234
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o. 5691155
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Pred. No. 1.23e+02
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5; Mismatches 1;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 12:43:10 1999; MasPar time 2.22 Seconds 153.061 Million cell updates/sec

ilar output not generated.

Description: Perfect Score: >US-08-599-226-32 (1-12) from US08599226.pep 78

Scoring table:

Sequence:

1 ASYLSTSSSLHY 12

PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 24.890; Variance 28.198; scale 0.883

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	No:
2221 2220 2221 2221 2221 2221	<u> </u>
	Score 52
55.4.1.1.5.5.5.5.8.8.8.1.1.1.4.4.4.4.4.4.4.4.4.4.4.4.4.4	Query Match
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	DB
YKRG_YEAST YKRG_YEAST YKRG_YEAST B4AR_MELGA YJF8_YEAST HPPD_ARATH CLPP_CHLEU PLTP_HUMAN POL1_BAYMG POL1_BAYMG DHSD_BOVIN B3AR_CAVPO B3AR_MOUSE B3AR_RAT B3AR_MACMU SECY_MYCTU PYRG_MYCLE IRE2_RAT	ID COX1 PHYPO
AL 93.4 KD AL 93.4 KD RENERGIC RE AL 60.8 KD AL 36.2 KD HENYLPYRUYA LIPP-LIKE PR ID TRANSFER ID TRANSFER IPP-CIKE PR ID TRANSFER ENERGIC REC ENERGIC R	Description
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POLR_TYMVC	YA9A_SCHPO	YT13_CAEEL	YBET_ECOLI	YW07_MYCTU	YRM8_CAEEL	YV18_MYCTU	COAT_ASFB7	YADC_SCHPO	KES1_YEAST	BENE_ACICA	HMP1_SHEEP	HMP1_PIG	HMP1_HUMAN	HMP1_MOUSE	HMP1_BOVIN	Y143_MYCGE	DP27_CAEEL	ERB2_HUMAN	CYGD_HUMAN	SOG_DROME	IRE2_HUMAN
RNA REPLICASE POLYPROT	HYPOTHETICAL 54.2 KD S	HYPOTHETICAL 48.6 KD P	20.9	HYPOTHETICAL 14.7 KD P	HYPOTHETICAL 216.3 KD	HYPOTHETICAL 57.3 KD P	MAJOR CAPSID PROTEIN (	HYPOTHETICAL 62.2 KD P	KES1 PROTEIN.	BENZOATE MEMBRANE TRAN	PITUITARY-SPECIFIC POS	HYPOTHETICAL PROTEIN M	CHROMOSOME CONDENSATIO	ERBB-2 RECEPTOR PROTEI	RETINAL GUANYLYL CYCLA	DORSAL-VENTRAL PATTERN	IRON-RESPONSIVE ELEMEN				
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EMBL; L14769; E101261;  PROSITE; PS00777; COX1; 1.  PRAM; PP00115; COX1; 2.  HSSP; P00396; 1OCC.  OXIDOREDUCTASE: HEME; COPPER; MITOCHONDRION; TRANSMEMBRANE;  RESPIRATORY CHAIN; INNER MEMBRANE.	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	SWISS-PROT entry is copyright. It is produced through a collaborativeen the Swiss Institute of Bioinformatics and the EMBL outstative Furnoces Bioinformatics Tatifacts Theory and the EMBL outstative Furnoces Bioinformatics	INTEGRAL MEMBRANE PROTEIN MITOCHONDRIA NS 12 POTENTIAL TRANSMEMBRANE DOMAINS. THE HEME-COPPER RESPIRATORY OXIDASE FA	AND COPPER B.  -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +  4 FERRICYTOCHROME C.  -!- DANHWAY: TERMITAI. GTED IN THE DESCRIPTION CUAIN	CHROME HEME A	THE REDUCTION OF OXYGEN TO WATER.  L CORE OF THE ENZYME COMPLEX. CO I	phalum.";	utional and inser	STRAIN=M3C; MEDLINE; 94064614.	[1] SEQUENCE FROM N.A.	MITOCHONDRION. EUKARYOTA; MYXOMYCETES; PHYSARIDA; PHYSARUM.	COXI. PHYSARUM POLYCEPHALUM (SLIME MOLD).	O1-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).	(REL. 33,	OX1_PHYPO STANDAR	T

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Best Local Similarity
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EMBL; 226878; G407504; -.
EMBL; 2268176; G4086310; -.
PIR; S34695; S34695.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 94205264.
WIEMANN S., VOSS H., SCHY
ZIMMERMANN J., GROTHUES [
ZIMMERMANN J., ANSORGE W.;
BANREVI A., ANSORGE W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKR6_YEAST
P34239;
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                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                    "VANDENBOL M., BOLLE P.-A., DION C., "Sequencing and analysis of a 20.5) arm of yeast chromosome XI."; YEAST 10:S25-S33(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequencing and analysis of 51.6 kilobases on the left arm of chromosome XI from Saccharomyces cerevisiae reveals 23 open reading frames including the FASI gene.";
YEAST 9:1343-1348(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FCB-1994 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL 93.4 KD PROTEIN IN STE3-GIN10 INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C;
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YKL176C OR YKL642
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                                    ASYLSTSSSLHY 12
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larity 66.7%;
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JES D., SENSEN
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ERFLE H., HEWITT
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PFAM; PF004400; G-beta; 5.
HYPOTHETICAL PROTEIN; REPEAT; WINEPEAT 73 103 WINEPEAT 114 144 WINEPEAT 157 187 WINEPEAT 205 235 WINEPEAT 248 278 WINEPEAT 248 278 WINEPEAT 248 34034 MW; 12
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P43141;
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YNL006W OR N2005.
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P41318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
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SUBMITTED (MAY-1996) TO I
-I- SIMILARITY: CONTAINS
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EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
"Molecular cloning receptor.";
                                                                                                                           BETA-4C ADRENERGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X77114; G496716; -.
EMBL; Z71282; E239859; -.
PIR; S45123; S45123.
PIR; S45461; S45461.
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yeast chromosome XIV, encompassing the centromere sequence.
YEAST 10:945-951(1994).
                                                                        MELEAGRIS GALLOPAVO (COMMON TURKEY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; MELEAGRIDIDAE; MELEAGRIS.
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Similarity 58.3%;
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Mismatches 2;
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             novel beta-adrenergic
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
11-100V-1997 (REL. 35, LAST ANNOTATION UPDATE)
11-10V-1997 (REL. 35, LAST ANNOTATION UPDATE)
11-10V-1997 (REL. 35, LAST ANDOTATION UPDATE)
11-10V-1997 (REL. 35, LAST ANDOTATION UPDATE)
11-10V-1997 (REL. 35, LAST ANDOTATION UPDATE)
11-10V-1997 (REL. 31, LAST ANDOTATION UPDATE)
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DOMAIN
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EMBL; U13978; G558882; -.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                          POHL T.M., ALJINOVIC G.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
-!- SIMILARITY: STRONG, TO YEAST YBR270C.
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N: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE.
ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF
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larity 40.0%;
Conservative
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BY SIMILARITY.
PALMITATE (BY SIMILARITY).
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STRAIR-K12 / MG1655;
MEDLINE 97426617.
MEDLINE F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
GREGOR J. DAVIS N.W., KI
MAU B., SHAO Y.;
   HPPD_ARATH
P93836; 0043
15-JUL-1998
15-JUL-1998
15-DEC-1998
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                                                                                                                                                                                                          EMBL; U18997; G606025; ALT_FRAME.
EMBL; U18997; G606026; ALT_FRAME.
EMBL; AE000390; G2367190; ALT_INIT.
ECOGENE; EG12729; YGJR.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
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BACTERIA; PROTEOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
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B.SUBTILIS YULF
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DAVIS N.W., KIRKPATRICK H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543
                                                                                                                                                                                      328 AA;
    (REL.
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(REL.
(REL.
1 36.2
                                                                                                                                           Conservative
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                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2 KD PROTEIN IN EBGC-UXAA INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                     BELONGS
36, CREATED)
36, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
                                                                                              12
                                                                                                                   77
                                                                                                                                                                                                   193
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                                                                                                                                                                 64.1%;
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J., GLASNER F.D., RODE C.K., MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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                                                                                                                                        Score 50; DB 1; 1
Pred. No. 6.49e+00,
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 1; I
Pred. No. 4.01e+00;
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                                                                                                                                                                                                  POTENTIAL
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                                                445
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                                                                                                                                                                                                                                                                                                                          There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                 GOEDEN M.A.,
                                                AA
                                                                                                                                                                                                                                                                                                                  as its content
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                                                                                                                                                               Length 328;
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MAYHEW G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  ROSE
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Best Local
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P42379;
01-NOV-1995
01-NOV-1995
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                     SEQUENCE FROM N.A. MEDLINE; 94329067. HUANG C., WANG S.,
                                                                                         CHLAMYDOMONADACEAE;
                                                                                                    EUKARYOTA; VIRIDIPLANTAE;
                                                                                                                   CHLOROPLAST
                                                                                                                             CHLAMYDOMONAS EUGAMETOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA I -!- CATALYTIC ACTIVITY: 4-HYDROXYPHENYLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSIEH T.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA
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NORRIS S.R., DELLAPE
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(IN) PLANT (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. WASSILEWSKIJA;
BARTLEY G.E., MAXWELL C.A.,
"Cloning of an Arabidopsis t
dioxygenase.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUPHYLLOPHYTES; SPERMATOP CAPPARALES; BRASSICACEAE;
"The Chlamydomonas chloroplast clpP gene contains translated insertion sequences and is essential for cell growth.";
                                                                                                                                                       PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
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                            LIU X.-Q.;
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                                                                                                                                                                                                                                                                                                                                  Cocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMOGENTISATE + CO(2).
COTACTOR: IRON (BY SIMILARITY).
PARTHWAY: PARTICIPATES IN THE CATABOLISM OF
PATHWAY FOR BIOSYNTHESIS OF PRENYLOUINONES.
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMIL
SIMILARITY: BELONGS TO THE 4HPPD FAMILY.
                                                                                                                                                                                                                                                                     ASYLSTSSSLHY
                                                                                                                                                                                                                                                                                                                                                                                 U89267; G2392518; -.
AF000228; G2145039; -.
AF047834; G3098559; -.
DREDUCTASE; DIOXYGENASE; IRON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                       CLPP-LIKE
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                                                                                                                                                                                                                                                                                                                                                                      445 AA;
                                                                                                                                                                  (REL.
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VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
TES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RODGERS
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JN-1997) TO
                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                    STANDARD;
                                                                                                                             32, CREATED)
32, LAST SEQUENCE UPDATE)
. 37, LAST ANNOTATION UPDATE)
. 37, CREASE (EC 3.4.21.92) (ENDOPEPTIDASE
                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                             97
                                        CHEN
                                                                                                                                                                                                                                                                                                                                64.1%;
58.3%;
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                                                                                         CHLAMYDOMONAS
                                     Ľ.,
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EMBL/GENBANK/DDBJ DATA BANKS
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                                                                                                    CHLOROPHYTA;
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                                                                                                                                                                                                                                                                                                                   Score 50;
Pred. No.
3; Misma
                                     LEMIEUX C.,
                                                                                                                                                                                                                                                                                                                                                                     B88784CA CRC32;
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6.49e+00;
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                                                                                                    CHLOROPHYCEAE; VOLVOCALES
                                       OTIS
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                                                                                                                                                                                                                                                                                                                                            Length 445;
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E + O(2)
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                                       TURMEL M.,
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Best Local S
Matches
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[2]
PROTEIN SPLICING.
PROTEIN SPLICING.
MEDLINE; 97277324.
SEQUENCE FROM N.A., AND SI
TISSUE-UMBILICAL VEIN END
MEDLINE; 94179366.
DAY J.R., ALBERS J.J., LOI
GRANT F.J., O'HARA P.J., N
                                                                                                                                                                                                                                             P55058;
01-OCT-1996
01-OCT-1996
01-NOV-1997
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ACT_SITE
SEQUENCE
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J. BIOL. CHEM. 272:11869-11873(1997).

-I- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS TO SMALL PEPTIDES:
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS TO SMALL PEPTIDES:
THE PRESENCE OF ATP AND MAGNESIUM. ALPHA-CASEIN IS THE USUAL SUBSTRATE. IN THE ABSENCE OF ATP, ONLY OLIGOPEPTIDES SHORTER.
FIVE RESIDUES ARE CLEAVED (SUCH AS SUCCINYL-LEU-TYR-I-NHMEC;
FIVE RESIDUES ARE CLEAVED (SUCH AS SUCCINYL-LEU-TYR-I-NHMEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00381; CLP_PROTEASE_SER; PROSITE: PS00382; CLP_PROTEASE_HIS; PROSITE: PS00881; PROTEIN_SPLICING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                      EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                       PLTP_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                    PRIMATES;
                                                                                                                                                                             HOMO SAPIENS
                                                                                                                                                                                                                         PHOSPHOLIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: THIS GENE CONTAINS TWO LARGE INSERTION SEQUENCES (IS1 AND CEU CLEP INTEIN) THAT DIVIDE THE CLEP GENE INTO THREE SEQUENCE DOMAINS. EACH INSERTION SEQUENCE FORMS A CONTINUOUS OPEN READING FRAME WITH ITS UPSTREAM AND DOWNSTREAM SEQUENCE DOMAINS. PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES A POST-TRANSLATIONAL EXCISION OF THE THE INTERVENING REGION (INTEIN) FOLLOWED BY PEPTIDE LIGATION.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY $14; ALSO KNOWN AS CLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY.
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PF00574; CLE____
EL; 2294; CHLeu; clpp; 1.
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                                                                                                                                  CATARRHINI; HOMINIDAE;
                                                                                                                                                      METAZOA; C
                                                                                                                                                                                                (REL. 34, CREATED)
(REL. 34, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
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904
419
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llarity 40.08;
Conservative
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1010
377
419
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                                                                ND SEQUENCE OF 18-27 ENDOTHELIAL CELLS;
LOFTON-DAY C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 1; I
Pred. No. 6.49e+00;
5; Mismatches 1
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CEU CLPP INTEIN
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W; D08E3DA6
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                                                                                                                                                      VERTEBRATA;
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FALSE_NEG.
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                    GILBERT T.L.,
                                                                                                                                                                                                                                                                                                                                       B
  ADOLPHSON J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SPLICING
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN 1 [CONTAINS: CYTOPLASMIC INCLUSION PROTEIN (CI);
RNA-DIRECTED RNA POLYMERASE (EC 2.7, 7.48); COAT PROTEIN (CP)].
BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1) (BAYMY).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
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CHAIN
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                                                                                                                                                                                                                                                                 KASHIWAZAKI S., MINOBE Y., OMURA T., HIBINO H.; "Nucleotide sequence of barley yellow mosaic virus evolutionary relationship with potyviruses."; J. GEN. VIROL. 71:2781-2790(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF01273; LI
LIPID TRANSPORT;
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or send an email to license@isb-sib.ch).
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-!- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION. PLACEN:
> LUNG > KIDNEY > HEART > LIVER > SKELETAL MUSCLE > 1
-!- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 91108371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q01206;
01-FEB-1994
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                     This SWISS-PROT entry
                                                                                                                           mosaic virus."
                                                                                                                                                               KASHIWAZAKI S.,
                                                                                                                                                                                                         MEDLINE; 90063549
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                              'Nucleotide sequence
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FUNCTION: CONVERTS HDL INTO LARGER AND SN
A KEY ROLE IN EXTRACELLULAR PHOSPHOLIPID
                                                            MAY BE INVOLVED IN REPLICATION.
                                                                                  EUNCTION: CYTOPLASMIC
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6; Mismatches
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1; C178FB86
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produced through a collaboration
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O1-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN 1 [CONTAINS: CYTOPLASMIC INCLUSION PROTEIN (CI);
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48); COAT PROTEIN (CP)].
BAKLEY YELLOW MOSAIC VIRUS (GERMAN ISOLATE) (BAYMY).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
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NP_BIND
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Q04574;
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PFAM;
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CHAIN
                                                                              PFAM; PF00680; RNA_dep_RNA_pol;
PFAM; PF00767; Poty_coat; 1.
PFAM; PF00863; Peptidase_C4; 1.
TRANSFERASE; RNA-DIRECTED RNA P
                                                                                                                                   PIR;
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                 PEERENBOOM E., PROELS M., SCHELL J., STEINBISS H.-H., DAVIDSO "The complete nucleotide sequence of RNA 1 of a German isolat barley yellow mosaic virus and its comparison with a Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; COAT PROTEIN; POLYPROTEIN;
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                                                                                                                                             EMBL; X69757; G58679; -.
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J1948; JQ1948;

M; PF00271; helica

M; PF00580; RNA_de

M; PF00767; POty_C

M; PF00863; Peptid
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CYTOPLASMIC INCLUSION PROTEIN
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RNA_dep_RNA_pol;
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                                                                            POLYMERASE; COAT PROTEIN; POLYPROTEIN;
 (POTENTIAL).
6BC96278 CRC32;
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Query Match

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Query Match
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15-DEC-1998 (REL. 37, CREATED)

15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUF

SUCCINATE OF CYBS) (SUCCINATE-UBIQUINONE REDUCTASE MEMBRANE)
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TRANSMEM
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SDHJ OR SDH4.
SDHD OR SDH4.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE-UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) (QPS3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHENOY S.K., YU L., YU C.A.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBMINT: COMPOSED OF A 27 KD IRON PROTEIN (IP), A
FLAVOPROTEIN (FP) AND A CYTOCHROME B COMPOSED OF
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BOS TAURUS (BOVINE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; BOVINAE;

BOVINAE;
PRIMATES; CATARRHINI;
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Q95123;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
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Pred. No. 1
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703D5238 CRC32;
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Mismatches 3;
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Best Local Similarity
Matches 5; Conser
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MEDLINE; 97151378.

ATGIE C., TAVERNIER G., D'ALLAIRE F., BENGTSSON T., MARTI L.,

CARPENE C., LAFONTAN M., BUKOWIECKI L.J., LANGIN D.;

"Beta 3-adrenoceptor in guinea pig brown and white adipocytes: low
expression and lack of function";

AM. J. PHYSIOL. 271:R1729-R1738(1996).

-!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF (
INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF (

INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF (

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Q1-NOV-1997
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"Cytochrome b in human complex II (succinate-ubiquinone oxidoreductase): cDNA cloning of the components in liver mitochondria and chromosome assignment of the genes for the large (SDHC) and small (SDHD) subunits to 1q21 and 11q23.";

CYTOCENET. CELL GENET. 79:132-138(1997).

-I- SUBUNIT: COMPOSED OF A 27 KD IRON PROTEIN (IP), A 70 KD FLAVOPROTEIN (FP) AND A CYTOCHROME B COMPOSED OF TWO INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
TRANSMEM
SEQUENCE
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01-NOV-1997 (REL. 35, LAST SEQUENCE UF
01-NOV-1997 (REL. 35, LAST ANNOTATION
BETA-3 ADRENERGIC RECEPTOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAVIA PORCELLUS (GUINEA PIG).
EUKARYOTA; METAZOA; CHORDATA;
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                    SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES.
THE GUINEA PIG DIFFERS FROM OTHER RODENTS BY AN ABSENCE OF I
ADRENERGIC EFFECTS AND BY LOW EXPRESSION IN BROWN AND WHITE
ADIPOSE TISSUES. IT IS CLOSER TO HUMAN OR PRIMATE THAN RODE!
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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159 AA;
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No. 1.67e+01
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Best Local S
Matches
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Ol-MAY-1992 (REL. 22, CREATED OL-FEB-1994 (REL. 28, LAST SE 15-JUL-1998 (REL. 36, LAST AN BETA-3 ADRENERGIC RECEPTOR. ADRB3 OR ADRB3R.
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DOMAIN
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        REVISIONS, SEQUENCE FROM N.A.

MEDLINE; 93779311.

VAN SPRONSEN A., NAHMIAS C., KRIEF S., BRIEND-SUTREN M.-M.,

STROSBERG A.D., EMORINE L.J.;

"The promoter and intron/exon structure of the human and mouse
                                                                            "Molecular characterization of relationship with the atypical EMBO J. 10:3721-3727(1991).
                                                                                                             NAHMIAS C., BLIN N.,
EMORINE L.J.;
                                                                                                                                                                                                                                                                                      B3AR_MOUSE
3-adrenergic-receptor genes.";
                                                                                                                                                STRAIN-SWISS;
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                             EUKARYOTA;
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                                                                                                                                                                                  RODENTIA;
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                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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COUPLED RECEPTOR;
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METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
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28, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                 MURIDAE; MURINAE; MUS.
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Pred. No. 1.67e+01;
5; Mismatches 1
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                                                                                     e beta 3-adrenergic receptor:
    of adipocytes.";
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HSSP; P07700; 1DEP.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
MULTIGENE FAMILY; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
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"PHARMACOL, 42:964-970(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCRDB; GCR_0253; -. GCRDB; GCR_0551; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93125503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THERMOGENESIS.
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S32804; S32804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
YLSTSSSLHY
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and human beta 3-adrenergic receptor genes contain
the protein-coding block.";
                                                                                                      Similarity
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                                                                                                                                                                     MW.
                                                                            Pred.
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Pred. No. 1.67e+01
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; 474A96AC
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Search completed: Thu Job time: 7 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 12:42:33 1999; MasPar time 3.14 Seconds 152.929 Million cell updates/sec

bular output not generated.

Description:
Perfect Score:
Sequence: >US-08-599-226-32 (1-12) from USUB599226.pep 78 1 ASYLSTSSSLHY 12

Scoring table: PAM 150 Gap 15

122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 24.334; Variance 30.685;

scale 0.793

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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beta-3-adrenergic rec	beta 3-adrenergic rec	н	beta-3-adrenergic rec	genome polyprotein 1	н	hypothetical protein	hypothetical protein	protein-export membra	protein-export membra	phospholipid transfer	Ig kappa chain precur		douridylate	otein - (	sensory transduction	probable purine nucle	beta-4C-adrenergic re		O	finger protein, Spl/e	apolipoprotein B - ra	Description
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5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	5.56e+01	3.63e+01	3.63e+0							

#accession	#journal #title	ACCESSIONS REFERENCE #authors	DATE	E N	Qy 3 YLSTSSSLHY	Db 175 YLQASTSLHY	Query Match Best Local Similarity Matches 7; Conse	#gene CLASSIFICATION SUMMARY	##residues 1-1 ##cross-references	##status	#cross-referen	#title	. ;	ACCESSIONS REFERENCE #authors		ISM	TITLE	1
specification and germ-rayer formation in brosophila. \$45336	Spl/egr_like zinc-finger protein required for endoderm	Chu-LaGraff, (	#ICCHMAL_Halle DIOSOPHILIA SP: 19-Mar-1997 #Sequence_revision 19-Mar-1997 #text_change 01-Aug-1997		LHY 12	LHY 184	75.6%; Score 59; DB 2; Length 989; larity 70.0%; Pred. No. 2.24e-01; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	apoB #superfamily apolipoprotein B #length 989 #checksum 1918	Type mkNA 1-989 ##label RES erences GB:M27440; NID:g623548; PID:g623549	preliminary; translated from GB/EMBL/DDBJ	peptides. cross-references MUID:89176719	Biosynthetic relationships between three rat apolipoprotein B		156333 Renben, M.A.: Svenson, K.L.: Doolittle, M.H.: Johnson, D.F.:	eb-1997	tus norvegicus #common_nam	apolipoprotein B - rat (fragment)	

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SUMMARY
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                                                                                           ##residues 1-306 ##label VA2
##cross-references EMBL:226878; NID:g407503;
##experimental_source strain S288C
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##molecule_type DNA
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##cross-references EMBL:228176; MIPS:YKL176c
##experimental_source strain S288C
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                                               #length
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                                                                                                                                                                                                                                                                                                                                                          submitted to the Protein $38006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wieman, S.; Voss, H.; Schwagaer, C.; Rupp, T.; Stegema Zimmermann, J.; Grothues, D.; Sensen, C.; Erfle, H.; Hewitt, N.; Banrevi, A.; Ansorge, W. submitted to the EMBL Data Library, July 1993 Sequencing and analysis of 51.5 kilobases on the left chromosome XI from Saccharomyces cerevisiae reveals reading frames including the FASI gene.
                                                                                                                                                                                                                                                                                                                                                                                                        Vandenbol, M.; Bolle, P.A.;
                                                                                                                                                                               S44583
                                                                                                                                                                                           Sequencing and analysis of a 20.5 kb DNA the left arm of yeast chromosome XI.
                                                                                                                                                                                                                             Yeast (1994) 10:25-33
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#formal_name Saccharomyces cerevisiae
30-Sep-1993 #sequence_revision 30-Sep-1993
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hypothetical protein YKL176c -
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No. 6.21e+00;
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6.21e+00;
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fle, H.;
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MIPS:YNL006w
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MIPS:YNL006w
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submitted
s62915
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#formal_name Saccharomyces cerevisiae
13-Jan-1995 #sequence_revision 27-Jan-1995
                                                                        A55044 #type complete
beta-{C-adreneryic receptor - turkey
#formal_name Meleagris gallopavo #common_name common turkey
18_Nov-1994 #sequence_revision 18-Nov-1994 #text_change
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#length 303
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Nucleotide sequence analysis of an 8887 bp region of the left arm of yeast chromosome XIV, encompassing the centromere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S45461 #type comp
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Pred. No. 9
3; Mismat
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9.75e+00;
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##molecule_type DNA
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                                                                         #authors Wang, N.; Shaulsky, G.; Escalante, Fjournal EMBO J. (1996) 15:3890-3898 #title A two-component histidine kinase guttitle Dictyostelium development.
#cross-references_MUID:96324397
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#residues 1-428 ##label CHE
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(Dictyostellum discoideum)
#formal_name Dictyostelium discoideum
29-Jan-1998 #sequence_revision 06-Feb-1998 #t
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probable membrane protein y1058c; protein J1141
#formal_name Saccharomyces cerevisiae
05-May-1995 #sequence_revision 08-Sep-1995 #text_change
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J. Biol. Chem. (1994) 269:24810-24819
Molecular cloning and characterization
beta-adrenergic receptor.
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>es EMBL:Z49333; NID:g1008200;
1-2150 ##label WAN
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Pred. No. 9.75e+00;
3; Mismatches 1
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Pred. No. 9.75e+00;
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Mol. Gen. Genet. (1994) 244:151-159
The Chlamydomonas chloroplast clpp gene contains large insertion sequences and is essential for
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autophosphorylation; phosphoprotein; phosphotransferase;
two-component regulatory system
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C1pp protein - Chlamydomonas eugametos chloroplast
#formal_name chloroplast Chlamydomonas eugametos
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_c)
01-Aug-1997
                              A71648
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#formal_name Rickettsia prowazekii
21-Nov-1998 #sequence_revision 21-1
21-Nov-1998
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                                                                              Nature (1998) 396:133-140
                                                                                                                        Andersson, S.G.E.; Zomorodipour, A.; Andersson, J. Sicheritz-Ponten, T.; Alsmark, U.C.M.; Podowski,
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                          #authors Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.;
#journal Biochem. J. (1992) 285:149-152
#title Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain precursors.
#cross-references MUID:92344562
#accession S24320
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##status
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##cross-references GB:AJ235273; GI
PID:g3861382
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##residues 1-33
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Similarity 60.0%;
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Ig kappa chain precursor - human
#formal_name Homo sapiens #common_name man
02-Dec-1993 #sequence_revision 17-Nov-1995
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ygjR
#superfamily Escherichia coli ygjR protein
#length 334 #molecular-weight 36990 #che
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science (1997) 277:1453-1462
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#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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#length 253
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               preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                            64.18;
41.78;
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Pred. No. 1.52e+
6; Mismatches
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Pred. No. 1.52e+01;
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1.52e+01
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Best Local S
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#title
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#accession A53533
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p_position 20pter-20qter
glycoprotein; phosphoprotein
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##cross-references EMBL:X64133; NID:g32810; PID:g32811
##note the authors translated the codon CAA f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **Status preliminary
##molecule_type mRNA
##rosid....
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Local Similarity 33.3%;
hes 4; Conservative
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1 ASYLSTSSSLHY 12
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Similarity 50.0%;
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phospholipid transfer protein precursor - human
lipid transfer protein II; PLTP
#formal_name Homo sapiens #common_name man
27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. (1994) Complete cDNA encoding
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                    Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
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Day, J.R.; Albers, J.J.; Lofton-Day, C.E.; Gilbert, T.I Ching, A.F.T.; Grant, F.J.; O'Hara, P.J.; Marcovina, Adolphson, J.L.
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heterotetramer; immunoglobulin
#length 135 #molecular-weight 14844 #checksum 5727
                                                                                                                                              #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 09-Aug-1997
12-Feb-1999
                                                                                                                                                                                                                    F64713 #type complete protein-export membrane protein -
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Richardson, D.; Dodson, R.; Knaıak, H
McKenney, K.; Fitzegerald, L.M.; Lee,
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s MUID: 04170266
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ces GB:L26232; NID:g468325;
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#product phospholipid transfer protein #status
experimental #label MAT
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Pred. No. 2.36e+
4; Mismatches
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Pred. No. 2.36e+01;
6; Mismatches 2;
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2.36e+01;
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ina, S.M.;
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Best Local Similarity 60.0%;
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Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
#journal Nature (1997) 388:539-547
#title The complete genome sequence of the gastric pathogen
#cross-references MUID:97394467
#accession F64713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal
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#cross-references MIID:99120557
#accession D71805
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##residues 1-503 ##label TOM
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##cross-references GB:AE001567; GB:AE001439; NID:g4156065; PID:g4156069
##experimental_source strain J99
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Local Similarity 60.0%;
hes 6; Conservative
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TIGR:HP1550
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T00353 #type fragment hypothetical protein KIAA0697 - human (fragment)
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Doily, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge,
B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
G.F.; Trust, T.J.
G.F.; Trust, T.J.
Nature (1999) 397:176-180
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#length 503 #molecular-weight 54247 #checksum 3320
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strain J99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cranslation not shown
                                                                                                                                                                                                                                                                                                                                               Score 49; DB 2; I
Pred. No. 2.36e+01;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 2; Leg
Pred. No. 2.36e+01;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein - Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 503;
                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pylori (strain
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                                                                                                                                                                                                                                                                                                                                                  Gaps
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Job time : 20 secs.

DATE

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TITLE

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GENETICS
#note
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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
DATE
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                                                                                           밁
Search completed: Thu Sep
                                                                                                                                                                                                      SUMMARY
                                                                                                                                             Query Match 62.8%;
Best Local Similarity 54.5%;
                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                           #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
                                                                                                                                                                                                                                                                                                                                                      #accession
                                                                                         653 SSYLPNSDPLH 663
                                                                                                                                                                                                                                                      ##cross-references EMBL:AB014597; NID:d1204352; PID:d1032633
##experimental_source brain; clone HK04486
                                                                                                                                                                                                                                                                                              ##residues
                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                    ##status
                                                       1 ASYLSTSSSLH 11
                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                  Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro. T00353
                                                                                                                                                                                                                                                                                                                                                                                                                        Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. DNA Res. (1998) 5:169-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Homo sapiens #common_name man
01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change
                                                                                                                                                                                                    #length 968 #checksum 7201
                                                                                                                                                                                                                       KIAA0697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T00353
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-Feb-1999
                                                                                                                                                                                                                                                                                              1-968 ##label ISH
                                                                                                                                                                                                                                                                                                                                  preliminary; translated from GB/EMBL/DDBJ
 2 12:42:53 1999
                                                                                                                                             Score 49; DB 2;
Pred. No. 2.36e+01
                                                                                                                                Mismatches
                                                                                                                              ?;
                                                                                                                                                              Length 968;
                                                                                                                              Indels
                                                                                                                              0
                                                                                                                              Gaps
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 12:43:36 1999; MasPar time 4.40 Seconds
148.939 Million cell updates/sec

ular output not generated.

Title: >US-08-599-226-32
Description: (1-12) from US08599226.pep
Perfect Score: 78

Scoring table: PAM 150 Gap 15 Sequence:

1 ASYLSTSSSLHY 12

ed: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl9

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_bhage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 24.038; Variance 31.822; scale 0.755

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

20 20 21 21 20 20 20	esult No.
4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	score
75 665 665 665 665 665 665 665 665 665 6	% Query Match
989 296 396 31 1238 1238 238 221 321 149 221 221 321 321 41 41 41 41 41 41 41 41 41 41 41 41 41	Length
11 11 11 11 11 11 11 11 11 11 11 11 11	DB
063052 Q26364 P911143 047582 061158 061158 077543 077543 077265 077267 070267	SUMMARIES
APOLIPOPROTEIN B  APOLIPOPROTEIN B  SIMILAR TO ACETYLTRANS  NADH DEHYDROGENASE SUB  F156.6 PROTEIN.  OLFACTORY RECEPTOR (FR  OLFACTORY RECEPTOR-LIK  OLFACTORY RECEPTOR-LIK  OLFACTORY RECEPTOR-LIK  OLFACTORY RECEPTOR (FR  OLFACTORY RECEPTOR (FR  OLFACTORY RECEPTOR  FROTEIN TYROSINE PHOSP  HISTIDINE KINASE A.  ZK1067.2 PROTEIN.  OLFACTORY RECEPTOR (FR  YÉEZA.6 PROTEIN.  P-HYDROXYPHENYLPYRUVAT  SIMILAR TO ACETYLTRANS  PROTEIN COMPLEX ASSEMB  SIMILAR TO FAMILY 1 OF  PROTEIN-EXPORT MEMBRAN  SIMILAR TO MATRIN F/G.	Description
4.42e-01 1.08e+01 1.0	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	17
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1943	1746	1101	932	725	646	613	463	435	285	265	198	185	122	98	1406	1046	910	349	301	204	176	176	1392	900
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062341	Q29116	Q22378	001623	Q52978	Q65281	074954	Q22925	P70033	002706	025144	075805	Q38688	P93302	018812	015082	P96156	059796	017959	Q22299	Q12097	Q36294	Q37837	082493	6/TC/0
PROTEIN.	TENASCIN PRECURSOR (TN	CODED FOR BY C. ELEGAN	SIMILAR TO LIGAND-GATE	PHA[A,B,C,D,E,F,G] GEN	MAJOR CAPSID PROTEIN.	HYPOTHETICAL 67.2 KD P	COSMID C50E3.	AR ORPHAN	PIT-1, PARTIAL (FRAGME	HROX1.	HOXA-9A.	LIGHT-HARVESTING CHLOR	ORF122A.	DELTA 3 PIT-1 (FRAGMEN	KIAA0377.	CHITODEXTRINASE.	PUTATIVE RECEPTOR ASSO	M01B2.5 PROTEIN.	T07C5.4 PROTEIN.	HYPOTHETICAL 22.6 KD P	CYTOCHROME B (FRAGMENT		T12H20.12 PROTEIN.	ALAMOSY PROTEIN (FRAG
	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01	9.00e+01			5.97e+01			5.97e+01		•	5.97e+01		J. YSE+UL

RESULT 2  ID Q26364; AC Q26364; DT Q1-NOV-1996 (TREMBLREL. Q1, CREATED) DT Q1-NOV-1996 (TREMBLREL. Q1, LAST SEQUENCE UPDATE) DT Q1-NOV-1998 (TREMBLREL. Q8, LAST ANNOTATION UPDATE) DE HKB-SEGMENTATION GAP-GENE HUCKEBEIN. GN HKB. QS DROSOPHILA MELANGGASTER (FRUIT FLY). QC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;	Query Match 75.6%; Score 59; DB 11; Length 989; Best Local Similarity 70.0%; Pred. No. 4.42e-01; Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Db 175 YLQASTSLHY 184     :	ID Q63052 PRELIMINARY; PRT; 989 AA.  AC Q63052; AC Q63052; DT 01-NOV-1996 (TREMBLREL. 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 08, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DE APOLIPOPROTEIN B (FRAGMENT). GN APOB. GN APOB. OC RATTUS NORVEGICUS (RAT). OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
Query Match 75.6%; Score 59; DB 11; Length 989; Best Local Similarity 70.0%; Pred. No. 4.42e-01; Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 175 YLQASTSLHY 184		

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  Query Match
Best Local S
Matches
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01-MAY-1997 (TREMBLREL. (
01-NOV-1998 (TREMBLREL. (
SIMILAR TO ACETYLTRANSFER
C37H5.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 3
P91143
P91143;
                                                                 WATERSTON R.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ
EMBL; U88315; G1825777; -.
PFAM; PF00561; abhydrolase; 1.
                                                                                                                                                                         STRAIN-BRISTOL N2;
DAVIDSON S., GILLAM I
SUBMITTED (FEB-1997)
                                                                                                                                                                                                                                                           WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of celegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and germ-layer formation in Drosophi
NATURE 369.664-668(1994).
EMBL; S71230; G547124; -.
FLYBASE; FBGR0001204; hkb.
PROSITE; PS00028; ZINC_FINGER_C2H2;
PFAM; PF00096; zf-C2H2; 3.
                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZINC-FINGER; METAL-BINDING; DNA-BINDING. SEQUENCE 296 AA; 33598 MW; 5716DF75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 94268555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTERYGOTA; DIP
DROSOPHILIDAE;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NATŪRE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHABDITINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JACKLE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRONNER G., CHU-LAGRAFF Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Spl/egr-like zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 APFLSAASDLYY 138
                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIPTERA; BRACHYCERA;
DAE; DROSOPHILA.
                                                       372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAZOA; NEMATO RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
llarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
  Conservative
                                                       Α
                                                                                                                                                                            ) TO
               58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEMATODA;
                                                       42139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03, CREATED)
03, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                            EMBL/GENBANK/DDBJ
                                                       WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITIDAE; PELODERINAE; CAENORHABDITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein required
in Drosophila.";
Score 52; DB 5;
Pred. No. 1.08e+01
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52; DB 5; L
Pred. No. 1.08e+01;
4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOE C.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                       5214F159 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COHEN B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC32;
                                                                                                          DATA BANKS
                                                                                                                                                                            DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 296;
                           Length 372;
  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endoderm specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEIGEL D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                        SHOWNKEEN
                                                                                                                                                                                                                                                                                                                                                                                           COULSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAUBERT
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  0
  Gaps
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 0;
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RESULT 5 II O61198 AC O61198; DT 01-AUG-1998 DT 01-AUG-1998 DT 01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches
                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MILLER N., STELLYES
SUBMITTED (DEC-1997
                                                                                                                                                             WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THLERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                047582
047582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TREMBLREL. 06, C: 01-JUN-1998 (TREMBLREL. 06, L. 01-JUN-1998 (TREMBLREL. 07, L. NADH DEHYDROGENASE SUBUNIT 5.
WATERSTON R.;
SUBMITTED (DEC-1997) TO EN
EMBL; AF038614; G2702437;
                                                                                                                                                                                                                                                                                                                                                          CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMAT
RHABDITINA; RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-FOREST;
KEDDIE E.M., UNNASCH T.R.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF015193; G2735946; -.
                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                  F15E6.6
                                                                                                                                                                                                                                                                                                                                                                                                             F15E6.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; FILARIOIDEA; ONCHOCERCIDAE; ONCHOCERCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONCHOCERCA VOLVULUS.
                                                                                                                                          NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 50.0% es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YLSTSSSLHY 12
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                                                                             (DEC-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                        (TREMBLREL.)
(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
                                                                                                                                                                                                                                                                                                                                                          NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
DIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62891
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08,
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06, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
               EMBL/GENBANK/DDBJ DATA
                                                                             BRADSHAW H., KEPPLER EMBL/GENBANK/DDBJ DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52;
Pred. No.
4; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
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                                                                              DATA BANKS
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                 BANKS
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RESULT
ID 07
AC 07
DT 01
DT 01
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                                               Query Match
Best Local S
Matches
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Best Local Similarity
Matches 5; Conser
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Best Local Similarity
Matches 7; Conser
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OLFACTORY RECEPTOR (FRAGMENT).
SUS SCROPA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
EUKARYOTA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                 01-NOV-1998 (TREMBLREL 08, CRI
01-NOV-1998 (TREMBLREL 08, LAX
01-NOV-1998 (TREMBLREL 08, LAX
0LFACTORY RECEPTOR (FRAGMENT).
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                       SEQUENCE FROM N.A.

MATARAZZO V., TIRARD A., RENUCCI M., BELAICH A.,

"Isolation of putative olfactory receptor sequence epithelium.";
                                                                                                                                                                                                               SUS SCROFA (PIG).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MATARAZZO V., TIRARD A., RENUCCI M., BELAICH A., CLE

"Isolation of putative olfactory receptor sequences
epithelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00197; 2FE2S_FERREDOXIN; 1. IRON-SULFUR.
SEQUENCE 1238 AA; 135726 MW; 9408B;
                                                                                                                    SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AF042017; G3273635; -...
NON_TER 1
                                                                                                                                                                                                                                                                                                                   077543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AF042016; G3273633; -.
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                                                                                               SEQUENCE
                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                         67
                                                          Local Similarity
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   ω
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                      YMAICSPLHY 76
 YLSTSSSLHY
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236 AA;
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238 AA;
                                               65.4%;
larity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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25822
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25564 MW;
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50.0%;
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70.0%;
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                               MW;
                                             Score 51; DB 6;
Pred. No. 1.68e+01
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 5; Pred. No. 1.08e+01 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 6;
Pred. No. 1.68e+01
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                                                                                               BEF1C7F3 CRC32;
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                                                                       Length 238;
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                                                                                                                                                                                J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pig nasal
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                                                                                                                                                                   pig nasal
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RESULT 8
ID 070265
AC 070265;
DT 01-AUG-1998 (TREMBLREL 07, CREATED)
DT 01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
DE CLEACTORY RECEPTOR-LIKE PROTEIN.

SCR D-8.
SCR D-8.
SCR D-8.
CRATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTOC SCIUROCONATHI; MURIDAE; MURINAE; RATTUS.

RR [1]
SCUURCE FROM N.A.
RC STRAIN-SPRAGUE-DAMLEY;
RX MEDLINE; 98211958.
RA WALENSKY L.D., RUAT M., BAKIN R.E., BLACKSHAW S., RONNE RA SNYDER S.H.;
RT "TWO novel odorant receptor families expressed in spern 5'-splicing";
RI 5'-splicing";
RI J. BIOL. CHBM. 273:9378-9387(1998).
EMBL; AF034887; G3153221; -
SQ SEQUENCE 321 AA; 35375 MW; D85F971F CRC32;
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SNYDER S.H.;
STWO novel odorant receptor families with the state of                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.4%;
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                               Matches
                                          ULT 10
088902;
088902;
088902;
01-NOV-1998 (TREMBLREL 08, CR.
01-NOV-1998 (TREMBLREL 08, LA.
01-NOV-1998 (TREMBLREL 08, LA.
PROTEIN TYROSINE PHOSPHATASE T
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070267;
070267;
01-AUG-1998
01-AUG-1998
01-NOV-1998
  PTP-TD14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-splicing.";
J. BIOL. CHEM. 273:9378-9387(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OLFACTORY RECEPTOR-LIKE PROTEIN. SCR D-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; MEDLINE; 98211958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNYDER S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WALENSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two novel odorant receptor
                                                                                                                                                                                                                                                                                                             129 YMAICSPLHY 138
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                   3 YLSTSSLHY
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NCE 321 A
NORVEGICUS (RAT).
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(TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                          Score 51;
Pred. No. 1
3; Mismat
                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
E TD14 (EC 3.1.3.48).
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Pred. No. 1.68e+01;
3; Mismatches 2
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                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   51; DB 11;
No. 1.68e+01;
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                                                                                                                                                                    1494
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Best Local S
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Best Local
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                                                                                                                                                                                                                                                          ULT 12
Q23388
Q23388;
Q13388;
Q1.NOV-1996 (TREMBLREL. 01, C
Q1.NOV-1996 (TREMBLREL. 01, L
Q1.JAN-1999 (TREMBLREL. 09, L
ZK1067.2 PROTEIN.
ZK1067.2.
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Q23863;
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WANG N., SHAULSKY G., ESCALANTE R., LOOMIS W.F.;
"A two-component histidine kinase gene that functions Dictyostellum development.";
EMBO J. 15:3890-3898(1996).
                                                                                                                                                    CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U42597; G1136289; -.

PFAM; PF00072; response_reg; 1.

PFAM; PF00512; s1gnal; 1.

SEQUENCE 2150 AA; 239662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
MEDLINE; 9836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel putative protein-tyrosine phosphatase domain and suppresses Ha-ras-mediated transform J. BIOL. CHEM. 273:21077-21083(1998).
EMBL: AF077000; G3598974; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAO
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SCIUROGNATHI;
                                    SUBMITTED
                                                                     THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHKA
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                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HISTIDINE KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYLSTSSSLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A
                                    (MAR-1996)
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HI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL. 01, (TREMBLREL. 01, (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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70.0%;
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                                    ö
                                EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 5; 1
Pred. No. 1.68e+01;
2; Mismatch-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENT ANNOTED
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02F946CE CRC32;
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No. 1.68e+01;
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                                DATA BANKS
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EMBL; Y08351; E273932; -
                                                                      045973 PRELI
045973;
01-JUN-1998 (TREM
01-JUN-1998 (TREM
01-JAN-1999 (TREM
Y6E2A.6 PROTEIN.
Y6E2A.6.
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BONFIELD J., BURTON J., CONNELL M., COPSRY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRRILLE P.,
LIGHTWING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATTSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P70013;
P70013;
01-FEB-1997
01-FEB-1997
  CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATO
RHABDITINA; RHABDITOIDEA;
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NON_TER
SEQUENCE
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01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-FACTORY RECEPTOR (FRAGMENT).
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA, METAKOA; CHORDOTA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 368:32-38(1994).
EMBL; Z70038; E1351037; -.
SEQUENCE 2219 AA; 253649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 96112032
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220 AA;
                                                                                                                         (TREMBLREL.) (TREMBLREL.
                                                                                                                                                                                                                            PRELIMINARY;
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50.08;
NEMATODA; SECERNENTEA; RHABDITII
DIDEA; RHABDITIDAE; PELODERINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24765
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                                                                                                                         96,6
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                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.58e+01;
2; Mismatches 3
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Pred. No. 1.68e+01
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  RHABDITIA; RHABDITIDA;
ODERINAE; CAENORHABDITIS.
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RA WEDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA WILSON R., AINSCOUGH R., CONSELL M., COPSEY T., COUPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAITSEER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMUURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA LIGHTNING J., LLOYD C., RIFKEN J., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RHIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAFERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RI 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT NATURE 368:32-38(1994).

EMBL: AL021175; E1350810; -.

SEQUENCE 357 AA; 40700 MW; 9B5AEA9E CRC32;
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conser
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Best Local Similarity 50.0%;
Matches 5; Conservative
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01-NOV-1998
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MEDLINE; 98369110.

NORRIS S.R., SHEN X., DELLA PENNA D.;

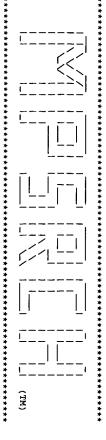
"Complementation of the arabidopsis pds1 mutation with the gene encoding p-hydroxyphenylpyruvate dioxygenase.";

PLANT PHYSIOL. 117:1317-1323(1998).
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
P-HYDROXYPHENYLPYRUVATE
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EUKARYOTA; VIRIDITLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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SEQUENCE FROM N.A.
MATTHEWS L.;
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58.3%;
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Pred. No. 2.58e+01;
4; Mismatches 1
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Pred. No. 2.58e+01;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Sep 2 12:46:53 1999; MasPar time 3.13 Seconds 153.392 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-599-226-33\_\_\_\_\_\_\_ (1-12) from US08599226.pep 74 1 ASFLSTSSSLEY 12

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

RESULT ENTRY TITLE

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: pir60 1:pir1 2:pir2 3:pir3 4:pir4 Mean 24.566; Variance 29.900; scale 0.822

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

#journal #title	#authors	REFERENCE	ORGANISM DATE	ENTRY TITLE
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotlin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caddwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galieron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Mosstl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T. M.; Portetelle, D.; Porwollk, S.; Prescott, A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Schleich, S.; Schroeter, R.; Socifone, F.; Schiguchi, J.; Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Tamakoshi, A.; Tanahaa, T.; Tarkemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanahaa, T.; Tarkemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanahaa, T.; Wanbutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Nature (1997) 390:249-256	Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;	D70048 A69580	#formal_name Bacillus subtilis 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998	D70048 #type complete ABC transporter (amino acid permease) homolog yvsH - Bacillus subtilis

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##molecule_type mRNA
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##residues 1-40
                         ##cross-references EMBL:AB006758; NID:d1227200; PID:d1033562
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Local Similarity 45.5%;
hes 5; Conservative
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Local Similarity 60.0%;
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BH-proteinerin-a - mouse
#formal_name Mus musculus #common_name house mouse
22-Jan-1999 #sequence_revision 22-Jan-1999 #text_cl
22-Jan-1999
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BH-protocadherin PCDH7 - human
#formal_name Homo sapiens #common_name man
22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change
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Genomics (1998) 49:458-461
                                                                                                 Yoshida, K.
submitted to the
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#length 469 #molecular-weight 50258 #checksum
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Pred. No. 2.14e+00;
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Pred. No. 2.14e+00;
5; Mismatches 1;
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##cross-references EMBL:AB006757; NID:d1184679; PID:d1026124
##exper1mental_source clone BH-Pcdh-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues
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                 Match 73.0%;
Local Similarity 60.0%;
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BH-protocadherin PCDH7 (clone BH-Pcdh-b) -
#formal_name Homo sapiens #common_name man
22-Jan-1999 #sequence_revision 22-Jan-1999
22-Jan-1999
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BH-protocadherin PCDH7 (clone BH-Pcdh-c) -
#formal_name Homo sapiens #common_name man
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              Score 54; DB 2;
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Pred. No. 2.14e+00;
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Pred. No. 2.14e+00;
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##cross-references GB:M60276; GB:M37764; NID:g151449; PID:g151453

Oxidoreductase
veight 60522 #checksum 6342
                                                                                                                                                                                                                           ##molecule_type DNA
##residnes
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##experimental_source strain S288C
There is no evidence that this sequence is expressed.
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J. Bacteriol. (1990) 172:6826-6833

Complete nucleotide sequence and polypeptide analysis multicomponent phenol hydroxylase from Pseudomonas s strain CF600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, 36.8 kb of S.cerevisiae chromosome PDC5, SLS1, PUT1 and tRNA-Asp.
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#length 112 #molecular-weight 13520
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#formal_name Saccharomyces cerevisiae
29.Nov-1995 #sequence_revision 05-Sep-1996 #text_change
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Pred. No. 3.44e+00;
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##molecule_type DNA
1-296 ##label BRO
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##residues 1-949 ##label LAM
##cross-references EMBL:AC004447;
#length 949 #checksum
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Local Similarity 58.3%;
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                                   S13808
S13807
                                                                                                                                        melanoma-inducing protein
                                                                                                                                                       $13808  #type fragment
protein-tyrosine kinase (EC 2.7.1.112) mrk (X chromosome)
southern platyfish (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broenner, G.; Chu-LaGraff, Q.; Doe, C.Q.; Cohen, B.; We D.; Taubert, H.; Jaeckle, H. Nature (1994) 369:664-668
Spl/egr-like zinc-finger protein required for endoderm specification and germ-layer formation in Drosophila. S45336
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S45336
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finger protein, Spl/egr-like
fformal_name Drosophila sp
19-Mar-1997_#sequence_revision
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#formal_name Homo sapiens #common_name man
23-Mar-1999 #sequence_revision 23-Mar-1999 #text_change
                                                                                                                    #formal_name Xiphophorus maculatus #common_name southern
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Adam, D.; Maeueler, W.; Oncogene (1991) 6:73-80
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21-Nov-1993
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Pred. No.
3; Misma
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Pred. No.
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1; M
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. No. 5.50e+00;
Mismatches 2;
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No. 1.38e+01
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5364
                 Schartl,
                                                                                    10-Nov-1995 #text_change
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Best Local Similarity 50.0%;
Matches 5; Conservative
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#introns
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#journal Oncogene (1991) 6:73-80
#title Transcriptional activation of the melanoma inducing
#title oncogene in Xiphophorus.
#cross-references MUID:91125882
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Local Similarity 50.0%;
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protein-tyrosine kinase (EC 2.7.1.112) mrk (Y chromosome)
southern platyfish (fragment)
melanoma-inducing protein
                      $313807 #type fragment protein-tyrosine kinase (EC 2.7.1.112) mrk present) - southern platyfish (fragment) melanoma-inducing protein
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21-Nov-1993 #sequence_revision 13-Mar-1997
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    #formal_name Xiphophorus maculatus
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th 346 #checksum 797
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th 311 #checksum 2822
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Pred. No. 1.38e+01;
4; Mismatches 1;
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Pred. No. 1.38e+01;
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    #common_name southern
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#title The complete genome sequence of Escherichia
#cross-references MUID:97426617
#accession B64970
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##residues 1-464 ##label BLAT
##cross-references GB:AE000295; GB:U00096; NID:g1788354;
#WGP:b2043
UWGP:b2043
UWGP:b2044
UWG
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##molecule_type 1-346 ##label
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Y #length 464 #molecular-weight 51315 #c
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##cross-references EMBL:X56317; NID:g65280; PID:g65281
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Local Similarity 50.0%;
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Local Similarity 45.5%;
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S13807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B64970 #type complete
hypothetical protein b2043 - Escherichia coli (strain K-
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
14-Nov-1997
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                      3-0-glucosyltransferase
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Pred. No. 1.38e+01;
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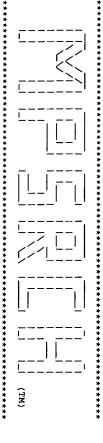
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REFERENCE $08324
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#journal Genetics (1988) 119:185-197
#title Sequence of three bornze alleles of maize and correlation
#title with the genetic fine structure.
#cross-references MUID:88284304
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##residues 1-471 ##label FUR
-##cross-references EMBL:X13501; NID:g22361; PID:g295854
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                                                                                                                                                                                                                                                                                                                                     $08325 #type complete flavonol 3-0-glucosyltransferase (EC 2.4.1.91) (allele BzMcC2) - maize UDPglucose flavonoid glucosyl-transferase #formal_name Zea mays #common_name maize 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 08-Sep-1997
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Sequence comparisons of three wild-type Bronze-1 alleles
Zea mays.
                                             #superfamily flavonol 03-glucosyltransferase
glycosyltransferase; hexosyltransferase
#length 471 #molecular-weight 48621 #check
                                                                                                                                                                                                                           Plant Mol. Biol. (1988) 11:473-481
Sequence comparisons of three wild-type Bronze-1 alleles from Zea mays.
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Search completed: Thu Sep 2 12:47:12 1999 Job time : 19 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm non:
Thu Sep 2 12:48:34 1999; MasPar time 1.45 Seconds 83.761 Million cell updates/sec

Tabular output not generated.

Title: >US-08-599-226-33

Description: (1-12) from US08599226.pep

Perfect Score: 74

Description: (1-12) from USO8599226.pe
Perfect Score: 74
Sequence: 1 ASFLSTSSSLEY 12
Scoring table: PAM 150
Gap 15

Searched: 106580 segs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Mean 16.342; Variance 51.433; scale 0.318

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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### ALIGNMENTS

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			Noland, Greta E.	NAME: Nolan	NA	റ്റ
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TYPE: amino actu
TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE 1026 AA; 111270 MW; 5f
70.3%; Sco.
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,003A
                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEPHAX: 312/984-9740
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino aci
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NAME: No. 5643781and, Gr
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 20 SOU
CITY: Chicago
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                                                                                                                 1026
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                                                                                                                PE: protein AA; 111270 MW;
                                                                                                                                     linear
                                                                                 70.3%;
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35,302
                                                                                 Score 52; DB 1; L
Pred. No. 3.63e+01;
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Pred. No. 3.63e+01;
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Best Local
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                                                                                        Sequence 95, Application US/08453274B
                                                                                                                                                     US-08-453-274B-95
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                                               Sequence 95, Application US/08453274B Patent No. 5663300 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
         APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocac NUMBER OF SEQUENCES: 107 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5708143and, Gret
REGISTRATION NUMBER: 35,30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Pr
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein PENCE 1026 AA; 111270 P
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
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TELLERAX: 25-3856
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                                                                                                                                                                                           FLSTSSSLEY 12
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CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
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ZIP: 60606
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  ADDRESSEE:
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VAL INFORMATION:
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5. 5708143
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llarity 50.0%;
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Marshall, O'Toole, Gerstein, Murray & Borun
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                    Protocadherin Materials and 107
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Best Local Similarity 50.0%;
Matches 5; Conservative
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application PC/TUS9312588 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 FLQTTTPLDY 432
                                                                                                              ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/1777
FILING DATE:
CLASSITET
                                                                                                                                                                                                        STREET: OCCUPANTE: Chicago
CITY: Illinois
THATE: ITSA
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PRINUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5663300and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,274B
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Suzuki, Shintaro
APPLICATION NUMBER: US 0 FILING DATE: 29 DEC 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & ADDRESSEE: Borun
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1026 AA; 111270 MW; 5611711 CN;
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6300 Sears Tower, 233 S. Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                              us 07/998,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52; DB 1;
Pred. No. 3.63e+01
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Best Local Similarity 50.0%;
Matches 5; Conservative
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                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5798224
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 95, Application US/08268161A Patent No. 5798224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 FLOTTTPLDY 432
                                                                                                                                             APPLICATION NUMBER: US/08/268,1
FILING DATE: June 27, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: YOUNG J. SUh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                       TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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LENGTH: 1026 amino acids
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                      STREET: 233 Sout
CITY: Chicago
STATE: Illinois
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1026 AA; 111270 MW; 5611711 CN;
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                      JE TYPE: protein
1026 AA; 111270 MW; 5611711 CN;
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70.3%; Score 52;
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TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
FRIGTH: 1203 amino acids
                    US-07-998-003A-103
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                                                                                              423 FLOTTTPLDY 432
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                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US93/12588
FILING DATE: 23 DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: NOLAND, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
                                                                      3 FLSTSSSLEY 12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08071
                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 1203 AA; 130280 MW; 7658453 CN;
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                       amino acid
GY: linear
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6300 Sears Tower, 233 S. Wacker Drive
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                                                                                                                                     70.3%;
50.0%;
                   STANDARD;
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                                                                                                                    Score 52; Db ,
pred. No. 3.63e+01;
pred. No. 3.63e+01;
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4; Mismatches 1;
                 PRT;
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                 1203 AA
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Best Local :
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                                                                                                                                               Sequence 103, Application US/08453695A
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                                                                               Patent No. 5708143
GENERAL INFORMATION:
APPLICANT: Suzuki.
                                                                                                                                                                                                                                                                                                          423 FLOTTTPLDY 432
                                                                                                           Sequence 103, Application US/08453695F Patent No. 5708143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5643781
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 103, Application US/07998003P Patent No. 5643781
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312/984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                 3 FLSTSSSLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,003A
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
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NAME: NO. 5643781and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                  APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocac
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1203 amino aci
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CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & ADDRESSEE: Bicknell
               ADDRESSEE:
                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                       LE TYPE: protein
1203 AA; 130280 MW; 7658453 CN;
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233 South Wacker, 6300 Sears Tower
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                            Marshall, O'Toole, Gerstein, Murray,
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                                                                Protocadherin Materials and Methods
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Pred. No. 3.63e+01;
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Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                                                                                          Sequence 103, Application US/08453274B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 FLOTTTPLDY 432
                                                                                                                                                                                                                                                                                       Patent No. 5663300
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        Sequence 103, Application US/08453274B Patent No. 5663300
      COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,274B
FILING DATE: 30-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5663300and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNET, O. 57084 3and, Greta E
NAME: No. 57084 3and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 3265
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 103:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                             APPLICANT:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1203 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
STATE:
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                                                                                                                                                            COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
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TELEX: 25-3856
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Illinois
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Pred. No. 3.63e+01;
4; Mismatches 1
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South Wacker Drive
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 103
SEQUENCE CHARACTERISTICS:
LENGTH: 1203 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                           MOLECULE TYI
SEQUENCE 1203
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Local Similarity 50.0%;
les 5; Conservative
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                                                                                                                                                                APPLICATION NUMBER: US 07/
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: NOland, Greta E.
REGISTRATION NUMBER: 35,30
REFERENCE/DOCKET NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 FLSTSSSLEY 12
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Protocadherin Materials NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                             TYPE: am-
TOPOLOGY: lin-
TOPOLOGY: lin-
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APPLICATION NUMBER:
                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                             TELEFAX: 51.
TELEFAX: 25-3856
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TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               ZIP: 60606
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STATE: Illinois
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70.3%;
llarity 50.0%;
Conservative
                                                                          amino acid
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                                           PE: protein
AA; 130280 MW; 7658453 CN;
                                                                  linear
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                                                                                                                                             312/474-6300
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                                                                                                                                                                                                                                                                   PCT/US93/12588
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Pred. No. 3.63e+01;
Score 52; DB 3; L
Pred. No. 3.63e+01;
4; Mismatches 1
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Best Local Similarity
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                  Sequence 11, Application US/08985090
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                                                                             US-08-985-090-11
                                                                                                                                                                                              SEQUENCE
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 103
SEQUENCE CHARACTERISTICS:
LENGTH: 1203 amino acids
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                                                                                                                                    423 FLOTTTPLDY 432
 Sequence 11,
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                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,10
FILING DATE: June 27, 1994
CLASSIFICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REGISTRATION NUMBER: 27866/
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Suzuki
                                                                                                                   3 FLSTSSSLEY 12
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MEDIUM TYPE: Floppy disk
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STREET: 22.
STREET: Chicago
CITY: Chicago
TATE: Illinois
USA
                                                                                                                                                                                            MOLECULE TYPE: protein
HENCE 1203 AA; 130280 MW; 7658453 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protoca
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                              60606
                                                                                                                                                        Conservative
Application US/08985090
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                                                                                                                                                                 70.3%;
                                                                             STANDARD;
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                                                                                                                                                                 Score 52; DB 2; I
Pred. No. 3.63e+01;
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Query Match
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                                                                                                                                                                   Sequence 2, Application US/08985090 Patent No. 5885893 GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5885893
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity tes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Andrew
                                                                                                                                                                                                                                                                                                                                                               3 FLSTSSSLEY
                                                                                                                                                                                                                                                                                                                                                                                         2 FLITASTLEF 11
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                 ARFULCANT: Andrew D.J. Goodearl TITLE OF INVENTION: MUSCARINTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 23 AA; 2719 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Andrew D.J. Goodearl TITLE OF INVENTION: MUSCARINIC
                                                                                                                                          NUMBER OF SEQUENCES:
                                                                             STREET: 28 St
CITY: Boston
STATE: Massac
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/985,090 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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CITY: Boston
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                                                                             Massachusetts
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Pred. No. 5.88e+01;
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

us/08/985,090

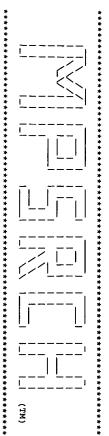
APPLICATION NUMBER: FILING DATE:

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Best Local Similarity 60.0%;
Matches 6; Conservative
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 445 AA; 48671 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION: FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application PC/TUS9507721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-07721-8
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application PC/TUS9507721 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 FLITASTLEF 207
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3 FLSTSSSLEY 12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street CITY: Atlanta
                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                       CLASSIFICATION:
                                                                                                                                                   FILING DATE:
                                                                                                                                                               APPLICATION NUMBER: PCT/US95/07721
                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                               Georgia
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 2; L
Pred. No. 5.88e+01;
3; Mismatches 1.
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Best Local S
Matches
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                                                                            263 APFMTPESSLEF 274
                                                                                                               Match 67.6%;
Local Similarity 50.0%;
                                                    1 ASFLSTSSSLEY 12
                                                                                                                                                                                                                      MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                   NAME/KEY: misc. feature LOCATION: 1.509
OTHER INFORMATION: /Func
                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                      6,
                                                                                                                                                     R INFORMATION: /Function = "Amino acid sequence for R INFORMATION: the murine Scavenger Receptor Class BI." 509 AA; 56754 MW; 1451442 CN;
                                                                                                      Conservative
             Sep
                                                                                                                                                                                                                                                 linear
              2 12:48:42 1999
                                                                                                    Score 50; DB 3; Length 509
Pred. No. 5.88e+01;
4; Mismatches 2; Indels
                                                                                                                            Length 509;
                                                                                                      0,
                                                                                                      Gaps
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993–1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm on:
Thu Sep 2 12:47:55 1999; MasPar time 4.49 Seconds 145.743 Million cell updates/sec

Title: >US-08-599-226-33

Description: (1-12) from USUB599226.pep
Perfect Score: 74

Sequence: 1 ASELSTSSSLEY 12

bular output not generated.

Scoring table: PAM 150 Gap 15

ırched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

sptrembl9

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 24.159; Variance 28.834; scale 0.838

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

20	18	17	16	15	14	13	12	11	10	9	80	7	σ	5	4	ω	N	1	Result
50	50	50	50	50	50	51	52	52	52	52	53	54	54	54	54	54	54	55	Score
67.6	57. 50	67.6	67.6	67.6	67.6	68.9	70.3	70.3	70.3	70.3	71.6	73.0	73.0	73.0	73.0	73.0	73.0	74.3	Query Match
503	346	311	296	198	60	649	1026	949	939	809	112	1200	1072	1069	1069	1035	469	475	Query Match Length
2	, <u>1</u> 3	13	σ	4	14	ω	4	4	4	տ	w	4	4	11	4	13	N	13	BG
026074	P11776	Q99162	Q26364	075805	Q69367	060167	Q08174	060369	015071	Q20702	Q07255	060247	060246	088185	060245	057537	032204	093514	ID
PROTEIN-EXPORT MEMBRAN	PROTO-ONCOGENE RECEPTO	MELANOMA RECEPTOR PROT	HKB-SEGMENTATION GAP-G	HOXA-9A.	GLYCOPROTEIN GG (FRAGM	PROTEIN COMPLEX ASSEMB	PROTOCADHERIN 42 PRECU	KIAA0365 (FRAGMENT).	KIAA0365 (FRAGMENT).	SIMILAR TO MATRIN F/G.	INTERNAL ORF OF L3149	PCDH7 (BH-PCDH)C.	PCDH7 (BH-PCDH)B.	BH-PROTOCADHERIN-A.	PCDH7 (BH-PCDH)A.	NF-PROTOCADHERIN.	YVSH PROTEIN.	AXIAL PROTOCADHERIN (F	Description
1.34e+01	1.34e+01	1.34e+01	1.34e+01	1.34e+01	1.34e+01	8.37e+00	5.19e+00	5.19e+00	5.19e+00	5.19e+00	3.20e+00	1.96e+00	1.96e+00	1.96e+00	1.96e+00	1.96e+00	1.96e+00	1.19e+00	Pred. No.

<b>4</b> 51	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
48	48	48	48	48	48	48	49	49	49	49	49	49	49	49	49	50	50	50	50	50	50	50	50	50
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1495	932	781	500	376	349	224	1476	890	664	643	516	509	442	303	155	662	599	593	511	511	509	509	509	509
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Q12280	001623	Q92071	Q41537	085449	017959	008247	Q90285	Q20388	022716	042633	Q52173	Q60417	050151	Q84594	051505	023064	Q80929	Q87093	032431	Q43981	088548	018824	P97943	Q61009
XVI READIN	SIMILAR TO LIGAND-GATE	INTEGRIN BETA3.	(SUBCLONE PAWJL218) AW	HYPOTHETICAL 42.6 KD P	M01B2.5 PROTEIN.	HSP18 TRANSCRIPTION RE	PUTATIVE EXTRACELLULAR	SIMILAR TO LIN-15B PRO	F8A5.30 PROTEIN.	FATTY ACID TRANSPORTER	PHENOL HYDROXYLASE P3	CD36-RELATED CLASS B S	UVRA PROTEIN.	1 SER	HYPOTHETICAL 18.1 KD P	BAC IG005I10.	REPLICATION PROTEIN E1	GLYCOPROTEIN G (HOMOLO	DMS OXYGENASE COMPONEN	OLHYDROXYLASE C		SCAVENGER RECEPTOR CLA	SCAVENGER RECEPTOR CLA	SCAVENGER RECEPTOR CLA
	3.37e+01		3.37e+01	3.37e+01		•	2.13e+01	2.13e+01	2.13e+01		2.13e+01	2.13e+01	2.13e+01	2.13e+01	2.13e+01	1.34e+01	1.34e+01	1.34e+01	1.34e+01	1.34e+01	1.34e+01	1.34e+01	1.34e+01	1.34e+01

### ALIGNMENTS

RP RN	8888	a D	g g	DT	AC	RESULT	Qy	Ф	Query Best Matcl	SQ	FΤ	FΤ	DR	Z :	33	7 5	RN	8	გ	S	GN	DE	ဌ	ď	Ŋ	ð	B	RESULT
[1] SEQUENCE FROM N.A. STRAIN-168;	BACILUS SUBTILIS.  BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; BACILLUS.		01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	(TREMBLREL. 05, CREAT	•	IT 2 O32204 PRELIMINARY; PRT; 469 AA.	3 FLSTSSSLEY 12	341 FLQTTTSLDY 350	Query Match 74.3%; Score 55; DB 13; Length 475; Best Local Similarity 60.0%; Pred. No. 1.19e+00; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	SEQUENCE 475 AA; 52268 MW; 2A681544 CRC32;			53469; G3598688;	D (MAR-1998) TO EMBL	"YODODING ARIAL DISCHOOLARING ".	FROM N.A.		INAE; XENOF	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;	XENOPUS LAEVIS (AFRICAN CLAWED FROG).	AXPC:	CADHERIN (FRAGMENT).	(TREMBLREL. 08, LAST ANNOTATION	(TREMBLREL. 08,	01-NOV-1998 (TREMBLREL. 08, CREATED)	••	O93514 PRELIMINARY; PRT; 475 AA.	in 1

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RESULT OF ACCORD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOR REPORTED RECEIVED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
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RA AZEVEDO V., GASAMARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTIERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA AZEVEDO V., BERTIERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BORLILLT S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA BORLISS R., BOURSIER L., BRAUN M., BRIGNELL S.C.,
RA BORLILLT S., BRUSCHI C.V., CALDWAINGS N.J., DANIEL R.A.,
RA CHOI S.K., CODANI J.J., CONNETTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA CHOI S.K., CODANI J.J., CONNETTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERIOFT A., EHRLICH S.D., EMMERSON P.T.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA GISEPPI G., GUY B.J., HACA K., HAIECH J., HARWOOD C.R., HENAUT A.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., KUMANO M.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA KURITA K., LAPIDUS A., LANDINOIS S., LAUBER J., LAZAREVIC V.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA PARRO V., POHL T.M., OGAWA K., OGIGWAR A., OUDEGA B., PARK S.H.,
RA PARRO V., POHL T.M., PORTETELLE D., PORWOLLIK S., PRESCOTT A.M.,
RA PESECAN E., PULICH S., SCHAPETER R., SCOFFONE F.,
SATO T., TEACHARD E., SCHLEICH S., FROHE B., ROSE M., SADAIE Y.,
SATO T., TANAKA T., TERPSTRA P., TOGNONI A.,
RA VIARI A., TACCONI E., TANAKA T., TERPSTRA P., TOGNONI A.,
RA VIARI A., YAMANOTO H., YAMANOE K., YASUMOTO K., YATA K.,
THE COMPLETE G., POHLER E., WEDLER H., WEITZENEGGER T.,
THE COMPLETE G., POHLER E., WEDLER H., WEITZENEGGER T.,
TATA CONTRACTOR H., TANAKA T., TERPSTRA P., TOGNONI A.,
THE COMPLETE G., POHLER E., WEDLER H., WEITZENEGGER T.,
TATA CONTRACTOR H., TANAKA T., YAMANOTO H., YAMANOE K., YASUMOTO K., YATA K.,
TATA CONTRACTOR H., TH
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Best Local S
Matches
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01-JUN-1998
01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O57537
        BRADLEY R.S., ESPESETH A., CURR. BIOL. 0:0-0(1998).
-!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                          XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ
EMBL; Z99121; E1186022; -
EMBL; AJ223978; E1249790; -
PFAM; PF00324; aa_permeases; 1.
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                                                                                                                                     SEQUENCE FROM N.A.
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(TREMBLREL.)
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EMBL/GENBANK/DDBJ DATA BANKS
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Pred. No. 1.96e+00;
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    (BY SIMILARITY).
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1- SUBCELLULAR LOCATION: TYPE I M.
1- SUBCELLULAR LOCATION: TYPE I M.
EMBL; AB006758; D1033562; -
PROSITE; PS00123; CADHERIN; 5.
CELL ADHESION; GLYCOPROTEIN; TRANS
CELL ADHESION; GLYCOPROTEIN; TRANS
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088185;
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01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
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GENOMICS 0:0-0(1998).
-I- SUBCELLULAR LOCATION: TYPE I
EMBL; AB006755; D1026122; -
PROSITE; PS00232; CADHERIN; 6.
CELL ADHESION; GLYCOPROTEIN; TRA
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O60245;
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01-AUG-1998 (TREMBLREL. (
01-AUG-1998 (TREMBLREL. (
PCDH7 (BH-PCDH)A.
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"Cloning, expression analysis, and chromosomal l
BH-protocadherin (PCDH7), a novel member of the
superfamily ";
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                          SUGANO S.; "cDNA cloning and chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS. MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
EUKARYOTA; MIRTDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCDH7
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PROSITE; PS00232; CAHERIN; 6.
CELL ADHESION; GLYCOPROTEIN; TRA
SEQUENCE 1035 AA; 113713 MW;
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YOSHITOMO-NAKAGAWA
                                                                                                                                                                                                                                                    YOSHIDA K., HIDA M.,
                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                              TRANSMEMBRANE;
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W; F1732B30 CF
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               VINEWBRANE; CALCIUM-BINDING; REPEAT
OF3F60C6 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SASAKI M.,
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Best Local Similarity
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01-AUG-1998 (TREMBLREL. (
01-AUG-1998 (TREMBLREL. (
01-AUG-1998 (TREMBLREL. (
PCDH7 (BH-PCDH)C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JLT 6
060246
060246; PRELIMINARY;
01-AUG-1998 (TREMBLREL 0
01-AUG-1998 (TREMBLREL 0
01-AUG-1998 (TREMBLREL 0
JLT 8
007255
007255;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                   YOSHIDA K., YOSHITOMO-NAKAGAWA K., SEKI N., SASAKI M., SUGANO S.; GENOMICS 0:0-0(1998).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; AB006757; D1026124; -.

PROSITE; PS00232; CADHERIN; 5.

CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT SEQUENCE 1200 AA; 130337 MW; 56F1CD33 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YOSHIDA K., YOSHITOMO-NAKAGAWA K., SEKI N., GENOMICS 0.0-0(1998).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PREMBL; AB006756; D1026123; -.
PROSITE; PS00232; CADHERIN; 6.
CELL ADHESION: GLYCOPROTEIN: TRANSMEMBRANE; SEQUENCE 1072 AA; 116463 MW; A3DF367C CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                       439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 FLHTSTPLDY 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 FLHTSAPLDY 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                                                                                             w
                                                                                                                                                                                    FLHTSTPLDY 448
                                                                                                                                                          FLSTSSSLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLSTSSSLEY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLSTSSSLEY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BH-PCDH)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
(TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.0%;
larity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.0%;
larity 60.0%;
Conservative
                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                      73.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07,
07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07, CREATED)
07, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; Depred. No. 1. 3; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.
3; Mismatc
                                                                                                                                                                                                                                            Score 54; DB 4; I
Pred. No. 1.96e+00;
3; Mismatches 1
CREATED)
LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                    112
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1.96e+00;
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1.96e+00;
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CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASAKI M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1072;
                                                                                                                                                                                                                                                 ۳.
                                                                                                                                                                                                                                                                                         Length 1200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUGANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT OF THE SULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                Query Match
Best Local S
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Best Local :
       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q20702;
Q20702;
01-NOV-1996
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOH
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.
LIGHTNING J., LLOYD C., MCMIRRAY A., MORTIMORE B., O'CALLAN
PARSONS J., PERCY C., RIFKEN L., ROOPA A., SAUNDERS D., S.
SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERST
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                     WATERSTON R.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; U40953; G1072256; -.
SEQUENCE 809 AA; 89741 MW; A01E9234 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILAR TO F53B1.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE) INTERNAL ORF OF L3149 PROBABLY NOT CODING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BRISTOL N2;
MILLER N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                           WATERSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHABDITINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELIUS H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "2.2 Mb of contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                    Local Similarity
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       6
                                                                                                                                                                                                                                                                                                                                                                                    (NOV-1995)
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6 (TREMBLREL.
8 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                    70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.6%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHABDITIDAE;
Score 52; DB 5; L
Pred. No. 5.19e+00;
4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 3; Pred. No. 3.20e+00
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PHAN H., VELASCO N., GARNES J., DANGANAN L., POUNDSTONE P.,
CHRISTENSEN M., GEORGESCU A., AVILA J., LIU S., ATTIX C., A.
TRANKHEIM M., AMICO-KELLER G., COEFIELD J., DUARTE S., LUCA.
BRUCE R., THOMAS P., QUAN G., KRONMILLER B., ARELLANO A.,
MONTGOMERY M., OW D., NOLAN M., TRONG S., KOBAYASHI A., OLS
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
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TANAKA A., KOTANI H., NOMURA N., OHARA,
"Prediction of the coding sequences of
The complete sequences of 100 new cDNA
code for large proteins in vitro.";
DNA RES. 4:141-150 (1997).
EMBL: AB002363; D1021661; -.
                                                                                               SUBMITTED (MAR-1998) TO ENEML; ACO04447; G2978447;
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01-NOV-1996 (TREMBLREL. 01, LAS;
01-NOV-1998 (TREMBLREL. 08, LAS;
01-NOV-1998 (TREMBLREL) 08, CAS;
PROTOCADHERIN 42 PRECURSOR (PC4
HOMO SAPIENS (HUMAN).
EUKARYOTRA; METRAZOA; CHORDATA; V
CATARRHINI; HOMINIDAE; HOMO.
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PROTEIN COMPLEX A
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 SCHIZOSACCHAROMYCETALES;
                                 SPBC19F8.03C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
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                  EUKARYOTA; FUNGI;
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SIMILARITY: BELONGS TO THE CADHERIN FRAMILY OF CELL ADHESION
MOLECULES. CONTAINS 7 CADHERINS-TYPE REPEATS.
ALTERNATIVE PRODUCTS: DIFFERENT FORMS OF THIS PROTEIN THAT DIFFER
AT THE C-TERMINUS ARE PRODUCED BY ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                    FLSTSSSLEY
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SCHIZOSACCHAROMYCETACEAE;
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X MEDLINE; 98290548.

X MEDLINE; OHANG H.H., SHIN C., CHO M., PARK D., PARK H. XI "GENOMIC STRUCTURE and sequence analysis of human HOXA DNA CELL BIOL. 17:407-414 (1998).

CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DR EMBL; U81511; 63237298; -.

DR PROSITE; PS00027; HOMEOBOX_1; 1

RW HOMEOBOX; NUCLEAR PROTEIN; DNA-BINDING.

KW HOMEOBOX; NUCLEAR PROTEIN; DNA-BINDING.

TOTHENCE 198 AA; 22874 MW; 307982CA CRC32;
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Best Local Similarity 36.4%;
Matches 4; Conservative
Query Match
Best Local Similarity
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Best Local Similarity 54.5%;
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01-NOV-1998
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SEQUENCE
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STRAIN=972H-;
STRAIN=972H-;
BECK A., REINHARDT R., WOOD V., RAJANDREAM M.A., BARRELL
BENTTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AL023594; E1293401; -
SEQUENCE 649 AA; 72985 MW; 9C207DB2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE; 93298054.

EBERLE R., ZHANG M., BLACK D.;

"Gene mapping and sequence analysis of simian herpesvirus SA 8 genome.";

ARCH. VIROL. 130:391-411(1993).

EMBL; L05608; G331077; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMIAN HERPESVIRUS SA8. VIRUSES; DSDNA VIRUSES, ALPHAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL 01, 01-NOV-1996 (TREMBLREL 01, 01-NOV-1998 (TREMBLREL 08, GLYCOPROTEIN GG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOXA-9A.
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2 SFLSTSSSLEY 12
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2 SFLSTSSSLEY 12
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GTREMBLREL.
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  67.6%;
41.7%;
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.34e+01;
7; Mismatches 0
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Pred. No. 8.37e+00;
Score 50; DB 4; Length 198; Pred. No. 1.34e+01;
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EMBL; X14112; G59562; -.
EMBL; X14112; G312376; -.
EMBL; X02138; G59870; -.
PIR; A05239; QQBE74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1.";

J. MOL. BIOL. 181:1-13(1985).
                                                                                                                                                PH4H_PSEAE STANDARD; PRT; 262 AA. P43334; P1334; P143334; P1501-NOV-1995 (REL. 32, CREATED) P1501-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) P1501-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
between the Swiss Institute of Bioinformatics and the Inthe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE; 94151331.
ZHAO G., XIA T., SONG J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                     PSEUDOMONAS.
                                                                                                                                                                                                                                                                                                                                                                   BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                   PSEUDOMONAS AERUGINOSA.
                                                                                                                                                                                                                                                                                                                                                                                                                 MONOOXYGENASE).
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66,
                                                                                                         SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                     PATHWAY: RATE-LIMITING STEP SUBUNIT: MONOMER.
                                                                                                                        SIMILARITY:
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THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
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larity 50.0%;
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                                                                                                                                                                                                                                                                          ROY R.A.;
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Pred. No. 2.36e+01;
5; Mismatches 0
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284A50FD CRC32;
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                                                                                                                                          PFAM; PF00351; biopterin_H; HSSP; P04177; lTOH.
                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                            EMBL; M88627; G476741; -
                       102 ATFIRTPEELDY
1 ASFLSTSSSLEY 12
                                              h 63.5%;
Similarity 41.7%;
5; Conservative
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262 AA;
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30288 MW;
                                             Score 47; DB 1; L
Pred. No. 2.36e+01;
4; Mismatches 3
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IRON (BY SIMILARITY).
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SDHD OR SDH4.
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HOMO SAPIENS (HUMAN).
""""" VERTEBRATA;
"""""TDAE; HOMO.
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014521;
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT
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                                                                                                                                            MITOCHONDRION;
                                                                                                                                                              TRICARBOXYLIC
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                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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01-NOY-1997 (REL. 35, LAST SEQUENCE UF
01-NOY-1997 (REL. 35, LAST ANOTATION
HYPOTHETICAL PROTEIN IN OLED 5'REGION
STREPTOMYCES ANTIBIOTICUS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA;
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GG OR US4.
HERPES SIMPLEX VIRUS (TYPE
VIRUSES; DSDNA VIRUSES, NO
                                             GLYCOPROTEIN
GG OR US4.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BIND
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE MALFG
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                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                               Theileria parva sporozoites.";
MOL. BIOCHEM. PARASITOL. 51:17-27(1992)
-i- SIMILARITY: BELONGS TO PEPTIDASE FA
PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92228011.
NENE V., IAMS K.P., GOBRIGHT E., MUSOKE "Characterisation of the gene encoding"
                                                                                                                                                                                                      HYDROLASE;
                                                                                                                                                                                                                 HSSP;
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Pred. No. 9.09e+00;
2; Mismatches 3
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2; Mismatches 2;
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Q1-NOV-1995 (
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CARBOHYD
                                                                                                                                                                                                    SHENOY S.K., YU L., YU C.A.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBUNIT: COMPOSED OF A 27 KD IRON PROTEIN (IP), A 70
FLAVOPROTEIN (FP) AND A CYTOCHROME B COMPOSED OF TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B
PRECURSOR (CYBS) (SUCCINATE-UBIQUINONE REDUCTASE M
GIBRINITM', CYCS')
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA;
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ASCOMYCOTA; ARCHIASCOMYCETES;

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TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WITTBRODT J., ADAM D., MALITSCHEK B., MAUELER W., RAULF F., TELLING A., ROBERTSON S.M., SCHARTL M.;
"Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu locus in Xiphophorus.";
NATURE 341:415-421(1989).

"IPPUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.

"IPPUNCTION: PROBABLE RECEPTOR WITH PROTEIN TYROSINE — ADD +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XIPHOPHORUS MACULATUS (SOUTHERN PLATYFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; ACTINOMORPHA;
                                                                                                                                                                                                                                                                    EMBL; X16891; G65291; -. PIR; S06142; S06142.
                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN TYROSINE PHOSPHATE.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 90015140.
                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Pred. No. 5.57e+00
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ATP (BY SIMILARITY).
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                      SIMILARITY.
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01-NOV-1997 (REL. 35, LAST SEQUENCE UI
01-NOV-1997 (REL. 35, LAST ANNOTATION
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                                                                          METAL
                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEIC ACIDS RES. 24:4420-4449(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCOPLASMA PNEUMONIAE. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIBONUCLEOSIDE-DIPHOSPHATE
                                                                                                                              PROSITE; PS00368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97105885
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                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: CONTAINS TWO IRON IONS (BY SIMILARITY).
PATHWAY: FIRST REACTION IN THE DNA REPLICATION PATHWAY
SUBURIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE CORRESPONDING RIBONUCLEOTIDES, PRECURSORS FOR DNA SYNTHESIS (BY SIMILARITY).
CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE DII
THIOREDOXIN + H(2)O = RIBONUCLEOSIDE DIPHOSPHA
                                                                                                                                                                                                                                                         veen the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE SMALL CHAIN FAMILY. MORE SIMILAR TO ENTEROBACTERIAL NE NRDB. SEEMS TO LACK TWO OF THE IRON-BINDING RESIDUES.
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SIMILARITY: BEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIOREDOXIN
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29342 / M129;
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                                                                                            DNA REPLICATION; IRON
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Pred. No. 5.
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Query Match

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Score 49;

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Length 339;

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01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE FLAVONOID
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MC2 ALLELE).
BZ1 OR UGT71A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence comparisons of 3 wild-type bronze-1 alleles from Zea m PLANT MOL. BIOL. 11:473-481(1988).
-!- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANI PIGMENTS.
-!- CATALYTIC ACTIVITY: UDP-GLUCOSE + A FLAVONOL = UDP + FLAVONOL - UDP-GLUCOSIDE.
-!- PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL STEPS IN THE ANTHOCYANIN BIOSYNTHETIC PATHWAY.
-!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
FURTEK D., SCHIEFELBEIN J.W., JOHNSTON
                                                                                                                                                                                                                        01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE FLAVONOID
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-W22 ALLELE).
BZ1 OR UGT71A1.
                                                                                                                                                                                                                                                                                                                                                 UFO3_MAIZE P16167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00201; UDPGT; 2.
TRANSFERASE; GLYCOSYLTRANSFERASE.
SEQUENCE 471 AA; 48621 MW; 3158C5E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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                                       SEQUENCE FROM N.A.

FURTEK D., SCHIEFELBEIN J.W., JOHNSTON

SEQUENCE comparisons of 3 wild-type by

PLANT MOL. BIOL. 11:473-481(1988).
                                                                                                                                                                                  ZEA MAYS (MAIZE).
EUKARYOTA; VIRIDIPLANTAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAIZEDB; 13885; -. PROSITE; PS00375; UDPGT; 1.
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or send an email to
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EMBL; U22831; G722359; -. WORMPEP; F47D12.7; CE01951. PFAM; PF00651; BTB; 1. PFAM; PF01344; Kelch; 6. HYPOTHETICAL PROTEIN; REPEAT. DOMAIN 387 566
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EMBL; X07937; G22210; -
PIR; S01037; S01037.
PIR; S08326; S08326.
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MAIZEDB; 13885; -.
PROSITE; PS00375; UDPGT; 1.
PFAM; PF00201; UDPGT; 2.
TRANSFERASE; GLYCOSYLTRANSFERASE.
TRANSFERASE; GLYCOSYLTRANSFERASE.
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01-FEB-1996
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-!- FUNCTION: IN THE PRESENCE OF CGLYCOSYLATION REACTION ALLOWS
                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                    SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N
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PATHWAY: ONE OF THE ESSENTIAL AND
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RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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Best Local (
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-i- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCI COLANIC ACID.
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01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPD
01-NOV-1997 (REL. 35, LAST ANNOYATION U
COLANIC ACID BIOSYNTHESIS PROTEIN WCAM.
ECOGENE; EG12651; WCAM.
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CONFLICT
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STRAIN-K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
BLATTNER F.R., PLUNKETT G. III, BLOCH G.A., PODE C.K., MAYHEW G.F.,
GREGOR J., DOLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AROMATIC HYDROCARBONS CATABOLISM; OXIDOREDUCTASE; FLAVOPROTEIN; FAD; IRON; PLASMID. SEQUENCE 517 AA; 60522 MW; FB61602A CRC32;
                                                                                                                            use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
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MEDLINE; 97251358.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEVENSON G., HOBBS M., ANDRIANOPOULOS K., REEVES P.;
"Organization of the Escherichia coli K-12 gene cluster responsible for production of the extracellular polysaccharide colanic acid.";
DACTERIOL. 178:4885-4893(1996).
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RALSTON E.J., ENGLISH J.J., DOONER H.K.;

"Sequence of three bronze alleles of maize and correlation with genetic fine structure.";

GENETICS 119:185-197(1988).

-i- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS,

-i- TUNCTION: REACTION ALLOWS THE ACCUMULATION OF ANTHOCYAN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
SEQUENCE
                                                                            MAIZEDB; 13885; -. PROSITE; PS00375; UDPGT; 1. PFAM; PF00201; UDPGT; 2. TRANSFERASE; GLYCOSYLTRANSFERASE.
                                                                                                                          EMBL; X13500; G1030071; -. EMBL; X07940; G22205; -. PIR; S01052; S01052. PIR; S08324; S08324.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A MEDLINE; 88284304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDD-GLUCOSE FLAVONOID
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MCC ALLELE).
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                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                 ANTHOCYANIN BIOSYNTHETIC PATHWAY.
-!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence comparisons PLANT MOL. BIOL. 11:47
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FURTEK D., SCHIEFE
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PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL STEPS IN
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SFLSTASSL
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm on:

Thu Sep 2 12:47:30 1999; MasPar time 2.21 Seconds 153.600 Million cell updates/sec

Title: >US-08-599-226-33 Description: (1-12) from US08599226.pep Perfect Score: 74

ular output not generated.

Sequence: 74
Sequence: 1 ASFLSTSSSLEY 12

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37

Statistics: Mean 25.085; Variance 27.334; scale 0.918

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	ATP-DEPENDENT CLP PROT	93.4 KD	HYPOTHETICAL 85.7 KD P	HEMAGGLUTININ PRECURSO	HEMAGGLUTININ PRECURSO	HYPOTHETICAL 59.0 KD P	CYTOCHROME C OXIDASE P	PHENYLALANINE-4-HYDROX	GLYCOPROTEIN G.	HYPOTHETICAL PROTEIN I	SUCCINATE DEHYDROGENAS	SUCCINATE DEHYDROGENAS	HYPOTHETICAL 54.2 KD S	CYSTEINE PROTEINASE PR	RIBONUCLEOSIDE-DIPHOSP	PRO	HYPOTHETICAL 66.0 KD P	FLAVONOL 3-O-GLUCOSYLT	FLAVONOL 3-O-GLUCOSYLT	FLAVONOL 3-O-GLUCOSYLT	COLANIC ACID BIOSYNTHE	PHENOL HYDROXYLASE P3	Description
3.75e+01		2.36e+01		2.36e+01		2.36e+01		2.36e+01	ü	2.36e+01	1.47e+01	1.47e+01			•		5.57e+00	5.57e+00			5.57e+00	2.05e+00	Pred. No.

EMBL; M60276; G151453; EMBL; D28864; G468469; PIR; D37831; D37831.

45	44	43	42	41	40	39	3 8	37	36	<u>3</u> 5	34	<b>ω</b>	32	31	30	29	28	27	26	25	24
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60.8	60.8	60.8	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2	62.2
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PHOSPHORIBOSYLAMINE G	HYDOTHETICAL 26 5 KD D	RAS-RELATED PROTEIN RA	HYPOTHETICAL 131.1 KD	DORSAL-VENTRAL PATTERN	KINESIN HEAVY CHAIN.	GLUTAMATE RECEPTOR PRE	HEPARAN SULFATE N-DEAC	BOX A-BINDING FACTOR (	LIN-19 HOMOLOG PROTEIN	HYPOTHETICAL 60.8 KD P	PROBABLE INTRON MATURA	PROTOPORPHYRINOGEN OXI	TUBULIN ALPHA CHAIN.	PROBABLE AMINOTRANSFER	LONGEVITY-ASSURANCE PR	ACYLNEURAMINATE CYTIDY	PUTATIVE 1-AMINOCYCLOP	PROTEIN A32.	PROTEIN A32.	N-TERMINAL ACETYLTRANS	PEPTIDYL-PROLYL CIS-TR
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# ALIGNMENTS

OLIPPILIPSESP STANDARD; PRT; 517 AA.  P1972; Ol-FEB-1991 (REL. 17, CREATED) Ol-FEB-1991 (REL. 17, CREATED) Ol-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) PHENOL HYDROXYLASE P3 PROTEIN (EC 1.14.13.7) (PHENOL 2-MONOOXYGENASE P) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) DMPN OR PHENAL PSEUDOMONAS SP. (STRAIN CF600).  BACTERIA: PROTEDRACTERIA. [1] SEQUENCE FROM N.A. MEDLINE; 91072230. NORDLUND I., POWLOWSKI J., SHINGLER V.; "Complete nuclectide sequence and polypeptide analysis of multicomponent phenol hydroxylase from Pseudomonas sp. strain SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-BH; TAKED M., MAEDA Y., OKADA H., MIYAMA K., MORI K., IKE M., "FUNTIAN M.; SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS '- FUNCTION: CATABOLIZES PHENOL, AND SOME OF ITS METHYLATED DERIVATIVES, P3 IS REQUIRED FOR GROWTH ON PHENOL, AND FOR JUNITY PHENOL HYDROXYLASE ACTIVITY COFACTOR: FAD FLAVOPROTEIN, AND REQUIRES FE(+2) FOR ACTIVITY COFACTOR: FAD FLAVOPROTEIN, AND REQUIRES FE(+2) FOR ACTIVITY COFACTOR: FAD FLAVOPROTEIN, AND PS POLYPEPTIDES SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED SUBMINT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED TO ACTIVITY PHENOL HYDROXYLASE ACTIVITY COFACTOR BY AND PROVINCE AND PROVINCE AND PROVINCE
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm on:

Thu Sep 2 12:51:38 1999; MasPar time 4.47 Seconds 146.610 Million cell updates/sec

Title: 

Description: (1-12) from USO8599226 pep

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9

"T'sp\_archea 2:5p\_bacteria 3:sp\_fungi 4:sp\_human

5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 24.013; Variance 31.833; scale 0.754

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score 58 57 53	Query Match 77.3 76.0 70.7		DB 3	ID 060167 026074 027336	Description PROTEIN COMPLEX ASSEMB PROTEIN-EXPORT MEMBRAN LET 858. VVSH PROTEIN
Match Length 77.3 649 76.0 503	ř.		2 3	ID 060167 026074	Description PROTEIN COMPLEX PROTEIN-EXPORT
70.7		897	σĸ	Q17336	LET 858.
69.	ω	469	N	032204	YVSH PROTEIN.
	'n	582	ω	074931	ALTERNATIVE NADH-DEHYD
69.	'n	1238	v	061198	F15E6.6 PROTEIN
	ö		N	051095	CONSERVED HYPOTHETICAL
68		349	ഗ	017959	M01B2.5 PROTEIN.
68			13	093514	AXIAL PROTOCADHERIN
68		932	ഗ	001623	SIMILAR TO LIGAND-GATE
66.7	. 7		9	048385	ORF83.
66.7	. 7		14	011696	NUCLEOPROTEIN (FRAGMEN
66	. 7		13	P70023	OLFACTORY RECEPTOR (FR
66	. 7	265	S	Q25144	HROX1.
66	. 7	372	տ	P91143	SIMILAR TO ACETYLTRANS
66	. 7	1186	14	055767	PUTATIVE TYROSINE PROT
65	٠.	122	10	P93302	ORF122A.
65	ί.	383	2	Q56675	MANNOSE-SENSITIVE
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	BH-PROTOCADHERIN-A.	RIN.	42 PF	PROTEIN B (F	U				COLICIN PROTEIN.	PHENOLHYDROXYLASE COMP	HYPOTHETICAL 52.8 KD P	SIMILAR TO ACETYLTRANS	NADH-UBIQUINONE OXIDOR	CONSERVED HYPOTHETICAL	HYPOTHETICAL 41.4 KD P	LSU	CHLOROPHYLL A/B ANTENN	PCB1, PCB2 AND PCB3 GE	ORF 27.	MELANOMA RECEPTOR PROT	GENE 27 PROTEIN.	KIAA0377.	KIAA0365 (FRAGMENT).
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### ALIGNMENTS

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HELICOBACTER. [1] SEQUENCE FROM N.A. STRAIN-26699; MEDLINE: 97394467.	HP1550. HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI). BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;	1998 (TREMBLEEL. 1998 (TREMBLEEL. -EXPORT MEMBRANE	(TREMBLREL. 05, CREATED)	LT 2 026074 PRELIMINARY; PRT; 503 AA.	2 SYLSTASSLEY 12	234 NYLSTARSLEF 244	Query Match 77.3%; Score 58; DB 3; Length 649; Best Local Similarity 72.7%; Pred. No. 7.07e-01; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	-	SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AL023594; E1293401;	BECK A., REINHARDT R., WOOD V., RAJANDREAM M.A., BARRELL B.G.;	SEQUENCE FROM N.A.		SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;	a	SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).	PROTEIN COMPLEX ASSEMBLY PROTEIN.	(TREMBLREL. 07, LAST ANNOTATIO	01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)	TORMET OFT 07	O60167 PRELIMINARY; PRT; 649 AA.	LT 1

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MATTHEWS L;
SUBMITTED (JUN-1998) TO EMB:
EMBL; U19615; G987227; -
EMBL; Z81525; E1351661; -
EMBL; Z81525; E1351661; -
EMBL; Z81525; AA; 104268
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                              01-JAN-1998
01-JAN-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
01-NOV-1996
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q17336
Q17336;
                            BACTERIA;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                          LET-835.

EUKARYOTA; BETAZOA; NEMATODA; SECERNENTEA; RHABDITI; EUKARYOTA; BHABDITOIDEA; RHABDITIDAE; PELODERINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHAANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHBRTY B.A. NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., MCKENNEY K., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M. COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WAITHEY L., WALLIN HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M., VENTER J.
                                                          YVSH.
                                                                                                              032204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; HP1550; -.
HYPOTHETICAL PROTEIN.
403 AA; 54247
                                                                                                                                                                                                                                                                                                                                          STRAIN-N2 (BRISTOL);
KELLY W.G., COLES L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of pylori[published erratum appears 25;389(6649):412].";
       SEQUENCE
                                               BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  GENETICS
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        LET-858.
                                                                                                                                                                                                                                                                                                                                                                                                                               LET 858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VENTER J
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                                                                     PROTEIN
                                                                                                                                                                    YLSTASSLEY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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       FROM
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                                      FIRMICUTES;
                                                                              B (TREMBLREL.
B (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TREMBLREL.)
(TREMBLREL.)
                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                           L.H.,
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80.
                                                                                                                                                                                                                        70.7%;
                                    BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
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9 %
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                                                                                EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                            FIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₩.;
                                                                                                                                                                                                                                                       WW;
                                                                                                                                                                                                            Score 53;
Pred. No. (
2; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                            A.Z.;
                                                                                                                          PRT;
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                                                                                                                                                                                                                                                      E1E3EA36 CRC32;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the gastric pathogen Helicobacter in Nature 1997 Sep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; DB 2; ]
No. 1.13e+00
                                                                                                                          469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    897
                                                                                                                                                                                                                        6.94e+00
                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC32;
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ODERINAE; CAENORHABDITIS.
                                                                              UPDATE)
                                                                                                                                                                                                                                 Length 897;
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., DOUGHERTY B.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local s
Matches
                                                                                                                                                                    074931;
074931;
01-NOV-1998
01-NOV-1998
                                                                                                             01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEREL. 08, LAST SANOTATION UPDATE)
ALTERNATIVE NADH-DEHYDROGENASE PRECURSOR (EC 1.6.5.3)
(NADH DEHYDROGENASE (UBIQUINONE)) (UBIQUINONE REDUCTASE)
(TYPE I DEHYDROGENASE) (COMPLEX I DEHYDROGENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KUNST F.,
                                 YARROWIA LIPOLYTICA (CANDIDA : EUKARYOTA; FUNGI; ASCOMYCOTA; DIPODASCACEAE; YARROWIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (FEB-1998) TO EMBL, EMBL; Z99121; E1186022; -. EMBL; AJ223978; E1249790; -. PFAM; PF00324; aa_permeases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98044033.
KUNST F., OGASAWAR
AZEVEDO V., BERTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 390:249-256(1997).
 SEQUENCE
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HARWOOD C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              376 TELTTAATLAY
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                                                                                                                                                                                                                                                                                                                             SYLSTASSLEY
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
5; Conser
FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OGASAWARA N
(NOV-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRIGNELL C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                  69.3%;
larity 45.5%;
Conservative
                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOSHIKAWA H., DAN
EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 52; DB 2; 1
Pred. No. 1.08e+01
5; Mismatches
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                                                       LIPOLYTICA).
; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49186162 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSE M.,
                                                                                                                                                                                                                                                 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DANCHIN
                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMMERSON P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 469;
                                                     SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DANCHIN A.;
terium Bacillus
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Best Local Similarity
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Best Local
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BONFIELD J., BURTON J., CONNELL M., COPREY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORFUNGRE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
F15E6.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WATSON A., WEINSTOCK L., WILKINS
"2.2 Mb of contiguous nucleotide
elegans.";
                                                                                                                                                                                                                             SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ EMBL; AF038614; G2702437; -. PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
MILLER N., STELLYES L.,
SUBMITTED (DEC-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THIERRY-MIEG J., THOMAS K., VAUDIN M., VAU
WATSON A., WEINSTOCK L., WILKINSON-SPROAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL; OXIDOREDUCTASE. SIGNAL 1 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHABDITINA;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                     ROSLLEUR.
IRON-SULFUR.
1238 AA;
                                             702 YLETQSSLNY 711
                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 TYLSAIASLGY
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  YLSTASSLEY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
582 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                           Conservative
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; 65814
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                                                                                                                 69.3%;
70.0%;
                                                                                                                                                                                      135726
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08,
                                                                                                                                                                                                                                                                                                                                                                                              BRADSHAW H., KEPPLER D.;
EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                         Score 52; DB 5;
Pred. No. 1.08e+01
1; Mismatches
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ALTERNATIVE NADH-DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0460C796
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                                                                                                                                                                                    9408BB7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; DB 3;
No. 1.08e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from chromosome
                                                                                                                                                                                                                                                                               DATA
                                                                                                                                    Length 1238;
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                                                                                           Indels
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Best Local
elegans";
elegans";
NATURE 368:32-38(1994).
EMBL; 283116; E1348127;
EMBL; 283116; A4011
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017959;
01-JAN-1998
01-JAN-1999
01-JAN-1999
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051095;
01-JUN-1998
01-JUN-1998
01-NOV-1998
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NATURE 390:580-586(1997).
NATURE 390:580-586(1997).
EMBL; ABC01120; G2687956; -.
EMBL; ABC068; -. 31278 MW
                                                                                                                 THIERRY-MIEG
WATSON A., WE
"2.2 Mb of co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ATCC 35210 / B31;

MEDLINE; 98065943.

FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.

LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., G

DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,

PETERSON J., KERLAVAGE A.R., OURKCENBUSH J., SALLBERG S., HANS

VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WELDMAN J.,

UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,

GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH
                                                                                                                                WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERY J., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA AINORE B., SOUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SOUSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAENORHABDITIS ELEGANS.
EHKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BORRELIA BURGDORFERI (LYME BACTERIA; SPIROCHAETALES; S
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMITH H.O., VENTER J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONSERVED HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHABDITINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M01B2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M01B2.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLOYD
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; BB0068; -.
293 AA;
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                                                                                                                 contiguous nucleotide
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(TREMBLREL.
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larity 70.0%;
Conservative
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06, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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SPIROCHAETACEAE; BORI
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Pred. No. 1
3; Mismat
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                        90870FE2 CRC32;
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                                                                                                              ON-SPROAT J., WOHLDMAN P. sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; DB 2; L
No. 1.67e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                   III of
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Best Local S
Matches
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Best Loc
Matches
                                                                                                 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M. DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VANGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          093514;
                                                                                                                                                                                                                                                                                                                                                                                       LT 10
001623
001623;
                                                                                                                                                                                                                                       STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                 CAENORHABDITIS ELEGANS.
EUKARYOTA; METAAOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TREMBLREL.
01-JUL-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
SIMILAR TO LIGAND-GATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Xenopus axial protocadherin.";
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AF053469; G3598688; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TREMBLREL. 08, CR
01-NOV-1998 (TREMBLREL. 08, LA
01-NOV-1998 (TREMBLREL. 08, LA
AXIAL PROTOCADHERIN (FRAGMENT)
                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                MURRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAMAMOTO
                  SUBMITTED
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 YLENSSGLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 FLOTTTSLDY
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Local Similarity 50.0%
tes 5; Conservative
                                                                                              .2 Mb of contiguous nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 YLSTASSLEY 12
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                  (APR-1997)
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475
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                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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52268
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50.0%;
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                 EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                      04, CREATED)
04, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
IONIC CHANNEL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST
LAST
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Pred.
3; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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1.67e+01;
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STRAIN-BRISTOL N2;
WATERSTON R.;
SUBMITTED (APR-1997) TO EMBL/GEN
EMBL; U97007; G1936466; -.
PFAM; PF00060; 11g_chan; 2.
SEQUENCE 932 AA; 106836 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (IRLEWING.).
NUCLEOPROTEIN (FRAGMENT).
MEASLES VIRUS (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MORBILLIVIRUS.
                                                                                                                           NON_TER
SEQUENCE
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011696
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NEVE H., ZENZ K.I., DESIERE F., KOCH A., HELLER K.J., BRUSSOW H.;

"Comparison of the lysogeny modules from the temperate Streptococcus
thermophilus bacteriophages TP-J34 and Sf121: implications for the
modular theory of phage evolution.";

VIROLOGY 241:61-72(1998).
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01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                 "Identification of three lineages sequence analysis of N, P, M, F, J. MED. VIROL. 52:113-120(1997).
EMBL: D87487; D1020995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TREMBLREL: 04, CREATED)
01-JUL-1997 (TREMBLREL: 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL: 08, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     011696;
01-JUL-1997
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                                                                                                                                                                                        NUCLEOPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 97278133.
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NCE 83 AA; 9876 MW;
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01-NOV-1996
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Q25144;
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"Two classes of olfactory receptors in
NEURON 15:1883-1392(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL.)
05 LAST ANNOTATION UPDATE)
01-FACTORY RECEPTOR (FRACMENT).
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
                                                                                                                                              FEBS LETT. 411:119-122(1997).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARI: EMBL; X75217; G407415; -.

PROSITE; PS00027; HOMEOBOX_1; 1.

PFAM; PF00046; homeobox; 1.

HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN.

SEQUENCE 265 AA; 29579 MW; B68A753D CRC32;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 97388321.

DEGNAN B.M., DEGNAN S.M., FENTENANY G., MORSE D.E.;

"A Mox homeobox gene in the gastropod mollusc Haliotis rufescens is differentially expressed during larval morphogenesis and metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HALIOTIS RUFESCENS (CALIFORNIA RED ABALONE) EUKARYOTA; METAZOA; MOLLUSCA; GASTROPODA; PALIOTIDAE; HALIOTIS.
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Local Similarity 70.0%;
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81 GSYLSMSSSKDY
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                                                  Similarity 58.3%, 7; Conservative
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222 AA;
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(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
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24658 MW;
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58.3%;
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                                               Score 50;
Pred. No. ;
3; Mismat
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Pred. No. 2.56e+01;
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                                                    Mismatches
                                          BREER H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
WILSON R., AINSCOUGH I
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P91143;
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EUKARYOTA; METAZOA; NEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SIMILAR TO ACETYLTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; U88315; G1825777; -.
PFAM; PF00561; abhydrolase; 1.
TRANSFERASE.
SEQUENCE 372 AA; 42139 MW; 5214F159 CRC32;
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DAVIDSON S., GILLAM B.;
SUBMITTED (FEB-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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                               12:52:11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITIDAE; PELODERINAE; CAENORHABDITI
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Pred. No. 2.
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2.56e+01;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

abular output not generated. n on: Thu Sep 2 12:51:12 1999; MasPar time 2.19 Seconds 155.131 Million cell updates/sec

Description: Perfect Score: Title: >US-08-599-226-34 (1-12) from US08599226.pep 75

Scoring table: PAM 150 Gap 15 Sequence:

1 ASYLSTASSLEY 12

77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 25.133; Variance 27.887; scale 0.901

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

sult No.	Score	% Query Match	Length	80	ID	Description	Pred. No.
1	51	68.0	1038	ㅁ ¦	SOG_DROME	DORSAL-VENTRAL PATTERN	4.04e+00
2	50	66.7	158	Н	DHSD_BOVIN	SUCCINATE DEHYDROGENAS	6.58e+00
ω	50	66.7	159	Ц	DHSD_HUMAN	SUCCINATE DEHYDROGENAS	6.58e+00
4	50	66.7	428	_	B4AR_MELGA	BETA-4C ADRENERGIC REC	6.58e+00
5	50		517	L	DMPN_PSESP		6.58e+00
σ	50	66.7	564	_	5HT1_DROME	5-HYDROXYTRYPTAMINE RE	6.58e+00
7	49		352	_	YDH3_SCHPO	HYPOTHETICAL 39.7 KD P	1.06e+01
- σο	49		441	Ц	SECY_MYCTU	PREPROTEIN TRANSLOCASE	1.06e+01
9	49		475	_	YM61_YEAST	HYPOTHETICAL 55.3 KD P	1.06e+01
10	49	65.3	917	_	GLRK_LYMST	GLUTAMATE RECEPTOR PRE	1.06e+01
11	48		272	-	YIGL_HAEIN	HYPOTHETICAL PROTEIN H	1.70e+01
12	48		471	_	UFO1_MAIZE	FLAVONOL 3-O-GLUCOSYLT	1.70e+01
13	48	٠	471	۳	UFO2_MAIZE	FLAVONOL 3-0-GLUCOSYLT	1.70e+01
14	48		471	ш	UFO3_MAIZE	FLAVONOL 3-0-GLUCOSYLT	1.70e+01
15	48	64.0	626	H	CEIB_ECOLI	COLICIN IB PROTEIN.	1.70e+01
16	48	64.0	1166	_	XMRK_XIPMA	MELANOMA RECEPTOR PROT	1.70e+01
17	48		1255	<u>, , , , , , , , , , , , , , , , , , , </u>	ERB2_HUMAN	ERBB-2 RECEPTOR PROTEI	1.70e+01
18	47	62.7	37	1	YRYL_CAEEL	HYPOTHETICAL 4.1 KD PR	2.71e+01
19	47	62.7	127	_	MBP_RAT	MYELIN BASIC PROTEIN S	2.71e+01
20	47		167	_	MBP_CAVPO	MYELIN BASIC PROTEIN (	2.71e+01
21	47	62.7	171	$\vdash$	MBP_PANTR	MYELIN BASIC PROTEIN (	•
22	47	62.7	194	1	MBP_MOUSE	MYELIN BASIC PROTEIN (	٠
23	47	62.7	196	_	MBP_HUMAN	MYELIN BASIC PROTEIN (	2.71e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	47
46	46	46	46	46	46	46	46	46	46	46	47	47	47	47	47	47	47	47	47	47	4/
61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	02./
1469	1023	824	753	554	505	483	416	413	341	301	848	697	684	653	577	530	485	399	339	330	202
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DP27_CAEEL	RT12_ACTPL	NPA2_HUMAN	YBHJ_ECOLI	NBL4_MOUSE	RADA_SYNY3	K1CL_MOUSE	YEIJ_ECOLI	DCHS_LYCES	CG2A_DAUCA	P34_RICRI	AMPN_LACLA	TRP_SCHPO	YV18_MYCTU	YJU4_YEAST	PYRH_YEAST	YA9A_SCHPO	G6PD_ZYMMO	HXAA_MOUSE	RIR2_MYCPN	ODBA_BACSU	I CCX LECOLL
CHROMOSOME CONDENSATIO	RTX-I TOXIN DETERMINAN	NEURONAL PAS DOMAIN PR	HYPOTHETICAL 81.5 KD P	NBL4 PROTEIN.	DNA REPAIR PROTEIN RAD	KERATIN, TYPE I CYTOSK	HYPOTHETICAL 43.4 KD P	HISTIDINE DECARBOXYLAS	G2/MITOTIC-SPECIFIC CY	PROTEIN P34.	AMINOPEPTIDASE N (EC 3	TRYPTOPHAN SYNTHASE (E	HYPOTHETICAL 57.3 KD P	HYPOTHETICAL 75.9 KD P	CTP SYNTHASE 2 (EC 6.3	HYPOTHETICAL 54.2 KD S	GLUCOSE-6-PHOSPHATE 1-	HOMEOBOX PROTEIN HOX-A	RIBONUCLEOSIDE-DIPHOSP	2-OXOISOVALERATE DEHYD	HIPOTHETICAL 24.1 ND P
4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	2.71e+01	2.71e+01	2.71e+01	2./Ie+UI							

# ALIGNMENTS

DR COR	88888888	8888888888888	R R T T R R R R R R R R R R R R R R R R	RES DT DT OS
og. 2. ENTAL PROTEIN; REPEAT; GROWTH FACTOR; AL-ANCHOR. CYTOPLASMIC (POTENTIAL).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	-!- FUNCTION: PUTATIVE NEGATIVE GROWTH FACTOR; ANTAGONIST OF DPP, A PROTEIN INVOLVED IN PATTERNING THE DORSAL REGION AND IN THE DEVELOPMENT OF THE NEUROECTODERM!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL)!- TISSUE SPECIFICITY: ABUTS THE DORSAL DPP-EXPRESSING CELLS IN A LATERAL STRIPE 14-16 CELLS WIDE. LATER IN EMBRYOGENESIS IT IS EXPRESSED IN NEUROECTODERM AND IN THE ENDODERM SPACED ALONG THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING GUT!- DEVELOPMENTAL STAGE: EMBRYOGENESIS!- SIMILARITY: CONTAINS 4 VWFC DOMAINS.	DIFTERA: BRACHYCERA; MUSCOMORPHA; EPHYDRO DAE; DROSOPHILA.  ROM N.A. 5047398. 7., SOLLOWAY M., O'NEILL J.W., EMERY J., BI intral patterning of the Drosophila embryo egative growth factor encoded by the short 8:2602-2616(1994).	RESULT 1  SCA_DROME STANDARD; PRT; 1038 AA.  AC 024025; DT 01-NOV-1997 (REL. 35, CREATED) DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) DE DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN).  GS SOG. SOG. SOG. SOG. SOG. SOG. DE DORSOPHILA MELANOGASTER (FRUIT FLY).  CC EUKARVOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;

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BOS TAURUS (BOVINE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; I

EUKARYOTA; RETAZOA; CHORDATA; PECORA; BOVOIDEA; BOVIDAE;
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SHENCY S.K., YU C.A.;
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SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- SUBUNIT: COMPOSED OF A 27 KD IRON PROTEIN (IP), A 70 KD
FLAVOPROTEIN (FP) AND A CYTOCHROME B COMPOSED OF TWO INTEGRAL
MEMBRANE PROTEINS.
-I- SUBCELLUAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE-UBIQUINONE REDUCTASE MEMBRANE ANCHOR
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1 155 SITCHONDRION (POTENTIAL).
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5; Mismatches
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"Cytochrome b in human complex II (succinate ubiquinone oxidoreductase): cDNA cloning of the components in liver and chromosome assignment of the genes for the large (SD (SDHD) subunits to 1q21 and 11q23.";

(STOGENET. CELL GENET. 79:133-138(1997).

-I-SUBUNIT: COMPOSED OF A 27 KD IRON PROTEIN (IP), A 70 FLAVOROTEIN (FP) AND A CYTOCHROME B COMPOSED OF TWO MEMBRANE PROTEINS.
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15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME E
PRECUBSOR (CYBS) (SUCCINATE-UBIQUINONE REDUCTASE
MELEAGRIS GALLOPAVO (COMMON TURKEY)
EUKARYOTA; METAZOA; CHORDATA; VERTE;
NEOGNATHAE; GALLIFORMES; MELEAGRIDI
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
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01-FEB-1991 (REL. 17, CREATED)

01-FEB-1991 (REL. 17, LAST SEQUENCE UI

15-JUL-1998 (REL. 36, LAST ANNOTATION

PHENOL HYDROXYLASE P3 PROTEIN (EC 1.14
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J. BIOL. CHEM. 269:24810-24819(1994).
J. BIOL. CHEM. 269:24810-24819(1994).
-!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE
-!- FUNCTION: GETA-ADRENYLATE CYCLASE THROUGH
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MEDLINE; 95014249.
CHEN X.-H., HARDEN T.K., NICHOLAS R.A.;
"Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U13977; G556604; -.
EMBL; U13978; G555882; -.
PROSITE; PS00237; G_PROTEIN_RECEPTOR;
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHT1_DROME STANDARD; PRT; 564 AA. P20905; 01-FEB-1991 (REL. 17, CREATED) 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) 5-HYDROXYTRYPTAMINE RECEPTOR 1 (5-HT RECEPTOR)
                                                                       activates adenylate cyclase.";

PROC. NATL. ACAD. SCI. U.S.A. 87:8940-8944(1990).

-I- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR

-I-SUNCYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION

AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF

THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a clotween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence and polypeptide analysis multicomponent phenol hydroxylase from Pseudomonas sp. CF600.";
                                                                                                                                                                                                                                                                                                                                                                                                            DROSOPHILA MELANOGASTER (FRUIT EUKARYOTA; METAZOA; ARTHROPODA; PTERYGOTA; DIPTERA; BRACHYCERA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; D37831; D37831.

AROMATIC HYDROCARBONS CATABOLISM; OXIDOREDUCTASE; FLAVOPROTEIN; FAD; IRON; PLASMID.
     ++
                                                                                                                                                                                                                                                                                 STRAIN=OREGON-R; : MEDLINE; 91062395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5HT-R1 OR 5-HT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M60276; G151453; -. EMBL; D28864; G468469; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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NORDLUND I., POWLOWSKI J., SHINGLER V.;
                                                                                                                                                                                                                                                       WITZ P., AMLAIKY N., PLASSAT J.-L.,
                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      DROSOPHILIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAKEO M., MAEDA Y.,
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                                                                                                                                                                                                                               'Cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 FLTAVSPLEY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIOL. 172:6826-6833(1990).
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  SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: FIRST STEP OF PHENOL BIODEGRADATION SUBUNIT: THE MULTICOMPONENT ENZYME PHENOL HYI BY P0, P1, P2, P3, P4 AND P5 POLYPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: FAD FLAVOPROTEIN, AND REQUIRES
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larity 50.0%;
Conservative
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                          INTEGRAL
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                                                                                                                                                                                                                               of a
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; TRACHEATA; HEXAPODA; INSECTA;
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No. 6.58e+00
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Drosophila
                          MEMBRANE PROTEIN
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                                                                     EN. THE ACTIVITY ACTIVATE ADENYL!
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HYPOTHETICAL 39.7 F
       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentilles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                      MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., CONNOR R.E. SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: SOME, TO YEAST YNL206C.
                                                                                                                                                                                              SPACEG9.03C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
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SEQUENCE
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-PROTEIN COUPLED RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLYBASE; FBgn0004573; 5-HT7.
PROSITE; PS00237; G_PROTEIN_RECEPTOR;
PFAM; PF00001; 7tm_1; 1.
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50.0%;
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PROTEIN C6G9.03C IN CHROMOSOME
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5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).
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9 X 2 AA TAN
BY SIMILARIT
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3 (POTENTIAL).
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MBL outstation -
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Best Local
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15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
15-DEC-1998 (REL. 3
                                                                             TRANSMEM
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SPECIES-M.BOVIS; STRAIN-BCG;
KIM J.K., CHOE Y.K.;
KIM J.K., CHOE Y.K.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH SECA-
TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLASMA
BY FORMING PART OF A CHANNEL (BY SIMILARITY).
-!- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY)
COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRI GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., BACHON S.V., EBALMA D., BROWN D., CHILLINGWORTH T., CONNOR R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., OLIVER S., OSBORNE J., QUALL M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON TAYLOR K., WHITEHEAD S., BARRELL B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; z81317; E276610; -. HYPOTHETICAL PROTEIN. SEQUENCE 352 AA; 39679
                                                                                                                        EMBL; U77912; G181 PROSITE; PS00755; PROSITE; PS00756;
                                                                                                                                                                  EMBL; AL021958; E1253270; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
NATURE 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 98295987
COLE S.T., BROSCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYCOBACTERIUM TUBERCULOSIS, AND MYCOBACTERIUM BOVIS. BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREPROTEIN TRANSLOCASE SECY SECY OR RV0732 OR MTV041.06.
                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTINOMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECY_MYCTU
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                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
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                                                                                          TRANSPORT;
                                                                                                                       PS00755; SECY_1;
PS00756; SECY_2;
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   18
57
78
124
157
180
                                                                                                          secY;
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77 TRANSMEMBRANE: TRANSLOCATION.
38 POTENTIAL.
77 POTENTIAL.
98 POTENTIAL.
144 POTENTIAL.
177 POTENTIAL.
177 POTENTIAL.
177 POTENTIAL.
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Pred. No. 1.06e+01
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01-NOV-1997 (REL.
01-NOV-1997 (REL.
HYPOTHETICAL 55.3 I
YMRZ11W OR YM8261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YM61_YEAST
Q03652;
Q1-NOV-1997
"Cloning subunit."
FEBS LETT
                                                                                    GLRK_LYMST STANDARD; PRT; 917 AA.
P26591;
01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
GLUTAMATE RECEPTOR PRECURSOR.
LYMNAEA STAGNALIS (GREAT POND SNAIL).
EUKARYOTT; METAZOA; MOLLUSCA; GASTROPODA; PULMONATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                        MEDLINE; 92070466.
HUTTON M.L., HARVEY R.J.,
"Cloning of a cDNA that e
                                                                                                                                                                                                                                                                                                                                EMBL; Z49809; G854463; -. PFAM; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-S288C / ABS
                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL PROTEIN
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                                                                                LYMNAEIDAE;
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                                                                                                                                                                                                                                                                                                           475 AA;
    292:111-114(1991).
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272
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382
                                                                                LYMNAEA.
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35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
KD PROTEIN IN RAR1-SCJ1 INT
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50.0%;
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                                     BARNARD
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Pred.
2; M
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                         an invertebrate
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No. 1.06e+01;
                                    E.A., DARLISON M.G
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                        glutamate receptor
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Best Local
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P44771;
01-NOV-1995
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DOMAIN
       FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRK KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MER MCKERNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDELOM E., COTTO WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDELOM E., COTTO
                                                                                                                BACTERIA; P. HAEMOPHILUS
                                                                                                                                        HAEMOPHILUS INFLUENZAE
                                                                                                                                                                         01-NOV-1995
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEMBRANE . SIGNAL
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WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M. UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON
                                                                                                                                                              HYPOTHET ICAL
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                                                                                           EQUENCE FROM
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                                                                                                                                                                                                                                                                    2 SYLSTASSLEY 12
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S15681; ACGAE.
S18443; S18443.
Crenno60; lig_chan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: L-GLUTAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM, THE POSTSYNAPTIC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                           Similarity
                                                                   υ / кw20;
95350630.
                                                                                                                           PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSTSYNAPTIC
                                                                                                                                                                        (REL.
(REL.
                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                CREATED)
                                                                                                                                                                        LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEMBRANE; IONIC
                                                                                                                                                                                                                                                                                                                                                              MW;
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Pred. No. 1.06e+01
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1; 879CBEDC CRC32;
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GLUTAMATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHANNEL; GLYCOPROTEIN;
                               CLAYTON R.A., KIRKNESS E.F.,
DOUGHERTY B.A., MERRICK J.M.,
ELDS C.A., GOCAYNE J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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R.C.,
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Best Local S
Matches
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PROSITE; PS01229; COF_2; 1
PFAM; PF00592; DUF3; 1.
HYPOTHETICAL PROTEIN.
SEQUENCE 272 AA; 30523
                                                                                                                                                                            MEDLINE: 88284304.

RALSTON E.J., ENGLISH J.J., DOONER H.K.

"Sequence of three bronze alleles of ma
genetic fine structure.";
GENETICS 119:185-197(1988).

-i- FUNCTION: IN THE PRESENCE OF OTHER
GLYCOSYLATION REACTION ALLOWS THE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MCC ALLELE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCIENCE 269:496-512(1995).
-i- SIMILARITY: BELONGS TO THE COF/:
(B.SUBTILIS) FAMILY. STRONG, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FINE L.D., FRITCHMAN GNEHM C.L., MCDONALD VENTER J.C.;
                                the
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 88284304.
                                                                                                                                                                                                                                                                                                              FURTEK D., SCHIEFELBEIN J.W., JOHNSTON F., NELSON O.E. "Sequence comparisons of 3 wild-type bronze-1 alleles PLANT MOL. BIOL. 11:473-481(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U32741; G1573586; TIGR; HI0597; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VENTER J.C.;
"Whole-genome random sequencing and
                                                           This
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      POACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ZEA MAYS (MAIZE).
EUKARYOTA; VIRIDIPLANTAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UFO1_MAIZE P16166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
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                                                                                 3-O-D-GLUCOSIDE.

PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL STEPS IN THE ANTHOCYANIN BIOSYNTHETIC PATHWAY.

SIMILARITY: BELONGS TO THE UDD-GLYCOSYLTRANSFERASE FAMILY.
                           ween the Swiss Institute of Bioinfo
                                                                                                                                                 CATALYTIC ACTIVITY:
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                                                                                                                                                                  PIGMENTS.
                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                         ZEA.
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                institutions as long
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                                                                                                                                              UDP-GLUCOSE + A FLAVONOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE COF/YBHA/YIDA/YIGL TRONG, TO E.COLI YIGL.
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Pred. No. 1.70e+01;
2; Mismatches 4
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               as its content
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                                                                                                                                                 UDP + FLAVONOL
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SIDA; POALES;
                                                                                                                                                                               ANTHOCYANIN
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EMBL; X07940; G22205; -
PIR; S01052; S01052.
PIR; S08324; S08324.
MAIZEDB; 13885; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE FLAVONOID
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MC2 ALLELE).
BZ1 OR UGT71A1.
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PROSITE; PS00375; UDPGT; 1.

PFAM; PF00201; UDPCT; 2.

TRANSFERASE; GLYCOSYLTRANSFERASE.

10760 Mil. 81
                                                                                                                              TRANSFERASE; GLYCOSYLTRANSFERASE.
SEQUENCE 471 AA; 48621 MW; 3158C5E0 CRC32;
                                                                                                                                                         PROSITE; PS00375; UDPOPERM; PF00201; UDPGT;
                                                                                                                                                                                                            EMBL; X13501;
PIR; S08325; S
                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FURTEK D., SCHIEFELBEIN J.W., JOHNSTON F., NELSON O.E. JR.;
"Sequence comparisons of 3 wild-type bronze-1 alleles from Zea mays."
PLANT MOL. BIOL. 11:473-481(1988).
-I- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZEA MAYS (MAIZE).
ZEA MAYS (MAIZE).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
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                                                                                                                                                                                                                                                                                                                                                                                          ANTHOCYANIN BIOSYNTHETIC PATHWAY.
SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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PATHWAY: ONE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: UDP-GLUCOSE + A FLAVONOL - UDP + FLAVONOL
                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - buropean Bioinformatics Institute. There are no restrictions on its produced institutions as long as its content is in no way the content is the content of the content is in no way the content is the content of the content is in no way the content is the content institutions as long as its content is in no way the content is the content institutions as long as its content is in no way the content institutions as long as its content is in no way the content institutions as long as its content is in no way the content institutions as long as its content is in no way the content institutions as long as its content is in no way the content institute.
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                                                              h 64.0%;
Similarity 88.9%;
8; Conservative
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Pred. No.
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No. 1.70e+01
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1.70e+01
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P16167;
01-APR-1990
                                                                                                        13-AUG-1987
13-AUG-1987
15-DEC-1998
COLICIN IB P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
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01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91) (UDP-GLUCOSE FLAVONOID
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-W22 ALLELE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEAM; PF00201; UDPGT; 2.
TRANSFERASE; GLYCOSYLTRANSFERASE.
SPOHENCE 471 AA; 48673 MW; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic fine structure.";
GENETICS 119:185-197(1988).
-!- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE: 88284304.
RALSTON E.J., ENGLISH J.J., DOONER H.
"Sequence of three bronze alleles of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FURTEK D., SCHIEFELBEIN J.W., JOHNSTON F., NELSON O.E. JR.; "Sequence comparisons of 3 wild-type bronze-1 alleles from Zea mays."; PLANT MOL. BIOL. 11:473-481(1988).
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ESCHERICHIA COLI.
PLASMID INCIl COLIB-P9.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAIZEDB; 13885; -. PROSITE; PS00375; UDPGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL STEPS IN THE ANTHOCYANIN BIOSYNTHETIC PATHWAY.

SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: UDP-GLUCOSE + A FLAVONOL -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOSYLATION REACTION ALLOWS
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PROTEIN.
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05, LAST SEQU
37, LAST ANNO
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MEDLINB: 85014128.

VARLEY J.M., BOULNOIS G.J.;

"Analysis of a cloned colicin Ib gene: complete nucleotide sequence and implications for regulation of expression.";

NUCLEIC ACIDS RES. 12:6727-6739(1984).
                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA and amino acid sequence analysis genes of colicins Ia and Ib.";
J. BACTERIOL. 168:228-236(1986).
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NUCLEIC ACIDS RES. 12:8748-8748(1984).

-!- FUNCTIO: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS CLASS OF TRANSMEMBRANE TOXINS DEPOLARIZE THE CYTOPLASMIC MEMBRANE, LEADING
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated. Thu Sep 2 12:50:40 1999; MasPar time 3.12 Seconds 154:181 Million cell updates/sec

Title: >US-08-599-226-34 (1-12) from US08599226.pep 75

Description:
Perfect Score:
Sequence: 1 ASYLSTASSLEY 12

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 24.614; Variance 30.527; scale 0.806

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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# ALIGNMENTS

RESULT 2 ENTRY	Db 38 YLSLASALEY       :    Qy 3 YLSTASSLEY	Query Match Best Local Similarity Matches 8; Conse	GENETICS #start_codon CLASSIFICATION SUMMARY	##molecule_type DN ##residues 1: ##cross-references	##status	#cross-refere	#journal #title					#authors	ACCESSIONS REFERENCE	ORGANISM DATE	RESULT 1 ENTRY TITLE
b71805 #type complete	YLSIASALEY 47       :    YLSTASSLEY 12	76.0%; Score 57; DB 2; Length 503; ilarity 80.0%; Pred. No. 6.18e-01; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	GTG #superfamily protein export membrane protein secD #length 503 #molecular-weight 54247 #checksum 3320	_type DNA 1-503 ##label TOM ferences GB:AE000652; GB:AE000511; NID:g2314720; PID:g2314730; TIGR:HP1550	<pre>preliminary; nucleic acid sequence not shown; translation not shown</pre>	cross-references MUID:97394467	Nature (1997) 388:539-547  The complete genome sequence of the gastric pathogen Helicobacter pylori.	Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujli, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.	McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;	J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;	Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,	Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;	F64713 A64520	<pre>#formal_name Helicobacter pylori 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 12-Feb-1999</pre>	F64713 #type complete protein-export membrane protein - Helicobacter pylori (strain 26695)

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ORGANISM
DATE
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#authors
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Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
24-Sep-1998
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#length 526
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Pred. No. 6.18e-01;
1; Mismatches 1
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#accession D70048
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                                                                                                                                     ##molecule_type DNA
##residues 1-293 ##label KLE
##cross-references GB:AE001120; GB:AE000783;
##CTOSS-references TIGR:BB0068
                                                                                                              ##experimental_source strain B31
Y #length 293 #molecula
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68.0%;
Similarity 70.0%;
7; Conservet'
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Similarity 45.5%;
5; Conservative
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Nature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bowman, C.; Garland, S.; Fuj
K.; Roberts, K.; Hatch, B.;
Nature (1997) 390:580-586
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                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence of a Lyme disease spirochaete, Borrelia
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#length 469 #molecular-weight 50258 #checksum 4200
                                                                                                                                                                                                                                                                                                                                 D70108
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                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown;
translation not shown
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Pred. No. 6.57e-
5; Mismatches
                                 Score 51; DB 2; Pred. No. 1.03e+01
        Mismatches
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6.57e+00;
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Best Local Similarity 58.3%;
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#title Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
#cross-references MUDD:99120557
                                                                                                                                                                                                                                                                                  #accession
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##cross-references GB:AE001487; GB:AE001439; NID:g4155086; PID:g4155090
##experimental_source strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 ATYRSTVANLEY 183
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##residues
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12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
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J99)
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#length 477 #molecular-weight 54625
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23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change
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il protein jhp0552 - Helicobacter
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#type complete
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o the EMBL Data
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Pred. No. 1.03e+01;
3; Mismatches 2
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Best Local Similarity 40.0%;
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##cross-references EMBL:X75217; NID:9407414; PID:9407415
#FICATION #superfamily unassigned homeobox proteins; hom
DNA binding; homeobox; nucleus; transcription
                                                                                                                                                                                                         122 YLAITAPLOY 131
                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-428 ##label
##cross-references GB:U13978;
                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
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D37831
A37831
                                                                                                                                                                                                                                                                                                   #superfamily vertebrate rhodopsin
neurotransmitter receptor; transmembrane protein
#length 428 #molecular-weight 47398 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A55044 #type complete
beta-4C-adrenergic receptor - turkey
#formal_name Meleagris gallopavo #common_name common turkey
18_Nov-1994 #sequence_revision 18-Nov-1994 #text_change
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larity 58.3%;
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#formal_name Haliotis rufescens #common_name California
                                            #formal_name Pseudomonas sp. 14-Jun-1991 #sequence_revision
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Pred. No. 1.62e+01;
5; Mismatches 1
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3; Mismatches 2
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NID:g555881; PID:g555882
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#title Cloning and characterization of a Drosophila serotonin
receptor that activates adenylate cyclase.
#cross-references MUID:91062395
#accession A38271
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##residues 1-517 ##label NOR
##cross-references GB:M60276; GB:M37764; NID:g151449; PID:g151453
                                                                                                                                                                                                                                                                           261 YLAITKPLEY 270
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the authors translated the codon CTT for residue 213
##note Ala, GTG for residue 215 as Leu, ATG for residue 28
as Leu and ATG for residue 551 as Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
##residues 1-564 ##label WIT
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serotonin receptor 7 - fruit fly (Drosophila melanogaster)
5-hydroxytryptamine receptor 7 (5-HTR7)
#formal_name Drosophila melanogaster
22-Jan.1993 #sequence_revision 22-Jan.1993 #text_change
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J. Bacteriol. (1990) 172:6826-6833

Complete nucleotide sequence and polypeptide analysis of multicomponent phenol hydroxylase from Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily octopamine receptor type I g protein: membrane protein;
 Bahr, U.; Tidona, C.A.; Darai, G. Virus Genes (1997) 15:235-245
The DNA sequence of Chilo irideso
                                                       Z14834
                                                                                                         703180 #type complete
tyrosine protein kinase homolog - Chilo iridescent virus
#formal_name Chilo iridescent virus
24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
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#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oilver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

#journal Nature (1998) 393:537-544

#cross-references MUID:98295987

#accession G70822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #gene
CLASSIFICATION
                                                                                                             ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.3%;
Best Local Similarity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g2911006
##experimental_source strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-1186 ##label BAH
##cross-references EMBL:AF003534; NID:92738385; PID:92738451
##cross-references EMBL:AF003534; NID:92738385; PID:92738451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 TYLSRESILDY 513
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                                                                                                                                                                                                                                                                                                                       309 GTYLSDPSNLVY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues 1-441 ##label COL
##cross-references GB:ALO21958; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
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Local Similarity 54.5%;
                                                                                                                                                                                                                                                                            1 ASYLSTASSLEY 12
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S55093
S55089
                                          #ypothetical protein YM8261.05
#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 01-Sep-
21-Nov-1997

      b/U822
      #type complete

      probable secY protein - Mycobacterium tuberculosis (strain H37RY)

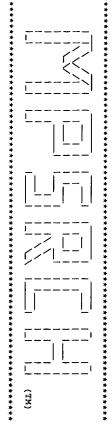
                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily preprotein translocase secy
#length 441 #molecular-weight 47611 #c
                                                                                                                                    hypothetical protein YMR211w - cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
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Pred. No. 1.62e+01;
2; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                         Score 49; I
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AL123456; NID:g3261536; PID:e1253270;
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2.52e+01
                                                                  01-Sep-1995
                                                                                                                                                          yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1186;
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Best Local Similarity
Matches 4; Conser
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Best Local 9
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559-578
599-617
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                                                                                                                                                                          62,95,121,125,229,
251,261,272,418,
419,424,491,881
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:x60086; NID:g9628; PID:g9629
IFICATION #superfamily glutamate receptor; glutamate receptor homology
RDS glycoprotein; ion channel; neurotransmitter receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 YLTTAITLGY 330
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##residues 1-917 ##label HUT
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##residues 1-475 ##label DED
##cross-references EMBL:249809; NID:g854459; PID:g854463; MIPS:YMR211w
                  729 AYLTESSTIDY 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 65.3%; Local Similarity 60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dedman, K.; Brown, D.; Bowman, S.
submitted to the EMBL Data Library, June 1995
$55093
                                                                                                                               predicted #length 917 #mo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #formal_name Lymnaea stagnalis #common_name great pond snail
#formal_name Lymnaea stagnalis #common_name great pond snail
31.Mar-1992 #sequence_revision 28-Oct-1994 #text_change
05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #length 475 #molecular-weight 55312 #checksum
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                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane protein
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                                                                                                                                                                                                                                #domain glutamate receptor homology #label GRH\
#domain transmembrane #status predicted #label TM1\
#domain transmembrane #status predicted #label TM2\
#domain transmembrane #status predicted #label TM3\
#domain transmembrane #status predicted #label TM4\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid sequence not
                                                                                                                                                                      #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                     #DOMAIN signal sequence #status predicted #label SIG\
#product glutamate receptor #status predicted #label
                                                                          65.3%;
36.4%;
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                                                                                                                                   #molecular-weight 103106 #checksum
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Pred. No. 2.52e+01;
2; Mismatches 2
                                                     Score 49; DB 1; Ler
Pred. No. 2.52e+01;
6; Mismatches 1;
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RESULT
ENTRY
TITLE
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Search completed: Thu Job time: 14 secs.
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                                                                                                                       475 FLSDENSLEY 484
                                                                                                                                                                                                                                             ##cross-references EMBL:AC004447; NID:g2978446; PID:g2978447

**Y #length 949 #checksum 5364
                                                                                                                                                                                                                                                                                       ##residues
                                                                                                                                                                                                                                                                                                            ##status
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Local Similarity 60.0%;
nes 6; Conservative
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                                                                                 3 YLSTASSLEY 12
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                                                                                                                                                                                                                                                                                                                        Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, K.; Gordon, L.; Kyle, A.; Ramirez, M.; Stilwagen, S.; Phan, H.; Velasco, N.; Garnes, J.; Danganan, L.; Poundstone, P.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, T.; Trankheim, M.; Amico-Keller, G.; Coefield, J.; Duarte, S.; Lucas, S.; Bruce, R.; Thomas, P.; Quan, G.; Kronmiller, B.; Arellano, A.; Montgomery, M.; Ow, D.; Nolan, M. submitted to the EMBL Data Library, March 1998 oseguence analysis of an -1 Mb region containing the MEF2B gene in 19p12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T03030 #type fragment
hypothetical protein KIAA0365 - human (fragment)
#formal_name Homo sapiens #common_name man
23-Mar-1999 #sequence_revision 23-Mar-1999 #text_change
23-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z14651
                  Sep
                                                                                                                                                                                                                                                                                       1-949 ##label LAM
                                                                                                                                                                                                                                                                                                          preliminary
                       2 12:50:54 1999
                                                                                                                                                             Score 49; DB 3; L
Pred. No. 2.52e+01;
2; Mismatches 2
                                                                                                                                                                                                     Length 949;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

ın on: Thu Sep 2 12:52:29 1999; MasPar time 1.40 Seconds 86.863 Million cell updates/sec

abular output not generated.

Description: Perfect Score: Title: >US-08-599-226-54 (1-12) from US08599226.pep 75 1 ASYLSTASSLEY 12

Scoring table: PAM 150 Gap 15 Sequence:

106580 seqs, 10152877 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: 

Statistics: Mean 16.154; Variance 53.667; scale 0.301

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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1255	1203	1203	1203	1203	1203	1203	1026	1026	1026	1026	1026	1026	445	290	290	23	426	426	159	158	117	37	Length
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20.	US-08-453-	US-08-453-	US-08-268-	US-07-998-	PCT-US93-1	PCT-US95-0	PCT-US93-1	US-08-453-	US-08-453-	US-07-998-	US-08-268-	PCT-US95-0	US-08-985-	US-08-420-	PCT-US95-1	US-08-985-	US-08-336-	PCT-US95-1	US-08-828-	US-08-828-	PCT-US96-0	PCT-US96-0	ID
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Description
68,	103	103	103	103	103	103	95,	95,	95,	95,	95,	95,		27,	27,	1,	-	2,	,	ω	11,	5	g
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	Sequence 2,	, 7	Sequence 17	Sequence 52	Sequence 7,	Sequence 4,	Sequence 5,	Sequence 40,	Sequence 2,	·		Sequence 1,	Sequence 33,	Sequence 2,	Sequence 68,	Sequence 68,	Sequence 2,	Sequence 68,		Sequence 2,
Applicatio	Applicatio		Applicati	Applicati	Applicatio	Applicatio	Applicatio	, Applicati	Applicatio	5194425.		Applicatio	, Applicati	Applicatio	, Applicati	, Applicati	Applicatio	, Applicati	Applicatio	Applicatio
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# ALIGNMENTS

8888888888888888	888888888888888	RESULT ID P AC XX XX XX XX XX XX XX XX XX XX XX CC CC
FILING DATE: 03-JUN-1996  CLASSIFICATION: ATTORNEY/AGENT INFORMATION:  NAME: Hendricks, Glenna REGISTRATION NUMBER: 32,535 REFERENCE/DOCKET NUMBER: PCT/US96/08730  TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 591-4470 TELEPAX: (703) 591-4478 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: unknown MOLECULE TYPE: peptide	NVENT NVENT SEQUE ENCE E EE: G E: G P.O. VA VA USA 031 EADAB YPE: IBJ YPE: IBJ YPE:	PCT-US96-08730-5 STANDARD; PRT; 37 AA.  xxxxxx  Sequence 5, Application PC/TUS9608730 Sequence 5, Application PC/TUS9608730 GENERAL INFORMATION: APPLICANT: Cassels, Frederick APPLICANT: Caster, John Mark

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                                                                                SEQUENCE
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                                 66.7%;
Local Similarity 58.3%;
hes 7; Conservation
                                                                                                                                                           TELEPHONE: (703) 591-4470
TELEFAX: (703) 591-4428
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 GSYLPTAVELTY 33
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                   22 GSYLPTAVELTY 33
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ANTI-SENSE: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08730
FILING DATE: 03-JUN-1996
                                                                              HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ENCE 117 AA; 12389 MW;
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PC
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carter, John Mark
TITLE OF INVENTION: Methods of Raising Antibodies Against E.
TITLE OF INVENTION: Coli of the Family CSF-CFA./1
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
                                                                                                                     MOLECULE TYPE:
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  ASYLSTASSLEY 12
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                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                 TOPOLOGY:
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P.O. Box 2509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cassels, Frederick
                                                                                                                               unknown
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NO
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58.3%;
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                                                                                                                                          single
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                                      Score 50; DB 3; L
Pred. No. 7.21e+01;
2; Mismatches 3
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                                                                                76297 CN;
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Sequence 1, Application US/08828832
                                     XXXXXX
                                                        US-08-828-832-1
                                                                                                                                                                       SEQUENCE
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                                                                                                               81 AAYLNPCSAMDY 92
                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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SOFTWARE: FASTEEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,832
FILING DATE: Herewith
CLASSTOTE
                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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APPLICANT: Shah, Purvi
TITLE OF INVENTION: NO
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                                                                                             ASYLSTASSLEY
                                                                                                                                                                                                                                 LENGTH:
TYPE: a
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ZIP: 94304
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CLONE: 1575011
                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
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                                                                                                                                  66.7%;
ilarity 41.7%;
Conservative
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Pred. No. 7.21e+01
5; Mismatches
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                                                                              Sequence 2, Application PC/TUS9513795
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                                                      Sequence 2, Application PC/TUS9513799 GENERAL INFORMATION:
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                                                                                                                                                                                                Match 66.7%;
Local Similarity 41.7%;
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.855-0555
                                                                                                                                                                          82 AAYLNPCSAMDY 93
                                                                                                                                                            1 ASYLSTASSLEY 12
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: Herewith
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTIME E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lal, Preeti
APPLICANT: Shah, Provi
TITLE OF INVENTION: NOVEL SUCCINATE DEHYDROGENASE SUBUNIT
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                        LENGTH: 159 amino TYPE: amino acid STRANDEDNESS: sing TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                CLONE: 2454416
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                                                                                                                                                                                                                        159 AA; 17043 MW; 129477 CN;
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                                                                                                                            STANDARD;
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Pred. No. 7.21e+01;
5; Mismatches 2
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Best Local Similarity
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                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (908) 594-6734
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 main acids
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESCEP.
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MOLECULE TYPE: protein
UENCE 426 AA; 47234 MW; 1032622 CN;
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOLLIS, GREGORY APPLICANT: PATEL, MAYUR D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                           STREET: 126 E. LI
CITY: RAHWAY
STATE: NEW JERSEY
                                                                                                                                                                                                                                                            ADDRESSEE: CHRISTAN ... ADDRESSEE: 126 E. LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
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07065-0900
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54.5%;
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Pred. No. 9.07e+01
4; Mismatches
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Matches 6; Consei
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Best Local Similarity
Matches 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08985090 Patent No. 5885893
                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                   TELEFAX: (617)742-444
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASYLSTASSLE 11
                                                                                                                                 NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MN
TELECOMMUNICATION INFORMATION:
TELECHONE: (617)227-7400
                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 23 AA; 2719 MW;
                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 426 AA; 47234 MW; 1032622 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Andrew D.J. Goodearl TITLE OF INVENTION: MUSCARINIC
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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   Conservative
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            64.0%;
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                                            3615 CN;
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 Score 48; DB 2; Ler
Pred. No. 1.14e+02;
3; Mismatches 1;
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Pred. No. 9.07e+01;
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                                Sequence 27, Application US/08420235B
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                                                                                                  US-08-420-235B-27
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application PC/TUS9510194
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Sequence 27, Application US/08420235B Patent No. 5801042
                                                                                                                                                                  100 PYLVTPSSIEF 110
                                                                                                                                                                                                                                                                          TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 amino acids
                                                                                                                                                                                                  Local Similarity
                                                                                                                                             2 SYLSTASSLEY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  MOLECULE TYPE: protein pence 290 AA; 32186 MW;
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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STREET: 11
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ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                : 290 amino acids
amino acid
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1185 Avenue of the Americas
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54.5%;
                                                                                                  STANDARD;
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                                                                                                                                                                                                 Score 48; DB 3; I
Pred. No. 1.14e+02;
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Best Local Similarity
Matches 6; Conser
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TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                US-08-985-090-2
                                                                                                                                                                                                              Sequence 2, Application US/08985090
                                                                                                                                                                                                                                                          XXXXXX
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                                                                                                                                                                             Patent No.
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                                                                                                                                                                                                                                                                                                                           SYLSTASSLEY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.25
CURRENT APPLICATION DATA:
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ENCE 290 AA; 32186 MW; 443934 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chang, Yuan
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                         TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
                                                                                                                                                       APPLICANT: Andrew D.J. Goodearl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/420,235B FILING DATE:
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                                                                 COUNTRY:
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PatentIn Release #1.0,
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Version #1.25
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 FLITASTLEF 207
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: US/08/985,090
        NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32149
TELECOMMUNICATION INFORMATION:
                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23 DEC
                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suzuki, Shintaro
                                                                                                                                                                                                                                              STREET: 6300 Sec
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                             CLASSIFICATION:
                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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445 AA; 48671 MW; 1062278 CN;
                                                                                                                                                                                                                             60606
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                                                                                                                                                                                                                                                                    6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.0%;
                                                                                             23 DEC 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                        PCT/US93/12588
                                                                                                                                                 PCT/US95/08071
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Pred. No. 1.14e+02;
3; Mismatches
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Best Local S
Matches
                                                                         TELEX: 25-3830
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                              MOLECULE TYPE: protein SEQUENCE 1026 AA; 111270 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-268-161A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 95, Application US/08268161A
423 FLQTTTPLDY 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 95, Application US/08268161A Patent No. 5798224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 FLOTTTPLDY 432
                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5798224
GENERAL INFORMATION:
                                                                                                                                    APPLICATION NUMBER: US/08/268,1
FILING DATE: June 27, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION UMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEFAX: 312/474-0448
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino aci
                    Local Similarity 40.0%; ses 4; Conservative
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3 YLSTASSLEY 12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1026 AA; 111270 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocac NUMBER OF SEQUENCES: 115
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & ADDRESSEE: Borun
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                    Score 48; DB 2; Ler
Pred. No. 1.14e+02;
5; Mismatches 1;
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Best Local :
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                                                       Sequence 95, Application US/08453695A
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                                                                                                                        US-08-453-695A-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 95, Application US/07998003A
Sequence 95, Application Patent No. 5708143
GENERAL INFORMATION:
APPLICANT: Suzuki, Sh
                                                                                                                                                                                        423 FLOTTTPLDY 432
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                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,003A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agtent No. JOJEPH PROPRIETON:
GENERAL INFORMATION:
GENERAL INFORMATION: Shintaro
APPLICANT: Suzuki, Shintaro
APPLICANT: TNVENTION: Protocadherin Materials and
                                                                                                                                                                                                              Local Similarity
nes 4; Conser
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                                                                                                                                                                    3 YLSTASSLEY
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 564378land, Greta
NAME: NO. 1564378land, Greta
NAME: NO. 1564378land, Greta
NAME: NO. 164378land, Greta
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                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEPHAX: 312/984-9740
                                                                                                                                                                                                                                                          MOLECULE TYPE:
JENCE 1026 AA
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
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CITY: Chicago
STATE: Illinoi:
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                                                                                                                                                                                                             64.0%;
llarity 40.0%;
Conservative
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AA; 111270 MW; 5611711 CN;
 Suzuki, Shintaro
                                                                                                                                                                                                                                                                              linear
                                                                                                                       STANDARD;
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                                 US/08453695A
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Pred. No. 1.14e+02
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5708143and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 3265
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 anios
                                                                                                                                                                                                                                                                                                                XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                               Sequence 95, Application US/08453274B
                                                                                                                                                                                                                           Sequence 95, Application US/08453274B Patent No. 5663300
                                                                                                                                                                                                                                                                                                                                                                                                               423 FLOTTTPLDY 432
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                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Suzuki
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,274B
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,695A
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CITY: Chicago
CTTY: Illinois
                                                                                                                                                              NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Pr
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                             STREET: 6300 Sec
CITY: Chicago
STATE: Illinois
                                                                                      COUNTRY: United States of America ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LE TYPE: protein
1026 AA; 111270 MW; 5611711 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.0%;
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Pred. No. 1.14e+02;
5; Mismatches 1;
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South Wacker Drive
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                                          Query Match
Best Local Similarity
Matches 4; Conser
                                                                                       SEQUENCE
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acidi
                    423 FLOTTTPLDY 432
3 YLSTASSLEY
                                                                                                                                                                                                           FILING DATE: 30-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5663300and, Greta E.
REGISTRATION NUMBER: 35,302
PROTECTION NUMBER: 32,302
                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                     TYPE: amino acid
                                                                                    LE TYPE: protein
1026 AA; 111270 MW; 5611711 CN;
                                          Conservative
                                                                                                                                 1026 amino acids
12
                                                                                                           linear
                                                     64.0%;
                                                     Score 48; DB 1; I
Pred. No. 1.14e+02;
                                                                                                                                                       95
                                          Mismatches
                                                              Length 1026;
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Search completed: Thu Sep 2 12:52:37 1999
Job time: 8 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:50:01 1999; MasPar time 3.46 Seconds 73.774 Million cell updates/sec

Title: >US-08-599-226-34

Description: (1-12) from US08599226.pep

Perfect Score: 75

Sequence: 1 ASYLSTASSLEY 12

Scoring table: PAM 150 Gap 15

earched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part4 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part44 35:part35 36:part36 37:part37 38:part38
39:part39

catistics: Mean 17.323; Variance 56.648; scale 0.306

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

11111111111111111111111111111111111111	Result
75 600 500 500 500 500 500 500 500 500 50	Score
100.0 96.0 93.3 99.3 89.3 85.3 86.0 80.0 80.0 77.3 77.3 776.0 76.0 76.0 76.0 76.0	Query Match
12 27 121 27 12 27	Length DB
7 W27593 W27588 7 W27589 7 W27592 7 W27591 7 W27591 7 W27586 7 W27587 7 W27587 7 W27587 9 W27587 9 W554260 9 W554260 9 W554260 9 W554260 9 W554260	B ID
Anti-TNF-alpha antibo Anti-TNF-alpha antibo	Description
antibo an	
4.20e 01 1.8.89e 01 1.4.6e-00 2.39e-00 3.06e+00 3.66e+01 1.66e-01 1.66e-01 1.66e-01 2.68e-01 2.68e-01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01 3.39e+01	Pred. No.

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38	19	19	18	9	9	19	27	19	39	œ	19	11	17	11	17	23	39	34	17	18	32	32	20	26	39	37	22	6
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.34e+0	.34e+0	.34e+0	.34e+0	.34e+0	.34e+0	.34e+0	.34e+0	.34e+0	.34e+0	2.68e+02	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.68e+0	.14e+0	.71e+0	.71e+0	.71e+0	./1e+0

## ALIGNMENTS

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                                                                                                                  PI Alien DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; PI Salfeld JG, Schoenhaut D, Vaughan TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer Claim 20; Page 73; 102pp; English.

CT The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity Cd determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or Cless and has a Koff rate constant of 1x10 power -3 s power -1 or Cless and has a Koff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmon resonance), and CC 1299 assay with an IC50 of 1x10 power -7 M or less. The Ab, which CC inhibits TNF-alpha activity, can be used to treat sepsis, CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid constitution, infectious diseases, malignancy, pulmonary, intestinal, CC sclerosis, autoimmune disbetes, autoimmune uveitis or nephrotic CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC alcoholic, viral or fulminant hepatitis, coagulation disturbances, CC alcoholic, viral or fulminant hepatitis, coagulation toxicity. The Ab also inhibits INF-alpha induced expression of endothelial cell call exhocyte adhesion molecule-1 (FIAM-1) on human umbilical vein
    Best Local Similarity
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Best Local Similarity 100.0%;
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25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TWF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-TNF-alpha antibody heavy chain CDR3; Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W27588 standard; peptide; 12
                                                                                       endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9729131-A1.
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                                                                                     leukocyte adhesion molecule-1 (ELAM-1)
endothelial cells (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human umbilical vein endothelial cell.
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                        Match
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; US-031476.
; US-599226.
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  96
  . 08;
  Score
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Pred.
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. No. 4.20e-01;
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  72;
No.
DB 27;
8.89e-01;
                                                                                                         on human
                    Length
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                                                                                                                                                                                             RESULT
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The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain variable region. The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro neutralises human TNF-alpha cytotoxicity in a standard in vitro 1p29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, ratery multiple sclerosis, autoimmune diseases, autoimmune uveltis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disease, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The health of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the prope
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Matches 1
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                                                                                 W27592 standard; peptide; 12
W27592;
19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukocyte adhesion molecule-1 (ELAM-1) endothelial cells (HUVEC).
Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High affinity antibodies against human TNF alpha TNF alpha activity, e.g. to treat autoimmune disease Claim 16; Page 76; 102pp; English.
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N-PSDB; T88404.
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-1997; U02219.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-TNF-alpha antibody heavy chain variable red
Human; tumour necrosis factor-alpha; TNF-alpha;
heavy chain; variable region; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W27569 standard;
W27569;
                                          Anti-TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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Similarity 90.9%;
10; Conservative
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antibody heavy chain CDR3. necrosis factor-alpha; TNF-
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Pred. No. 1.46e+00;
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   TNF-alpha; antibody; CDR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on human umbilical vein
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High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer PS Claim 20; Page 74; 102pp; English.

THF alpha activity, e.g. to treat autoimmune diseases and cancer PS Claim 20; Page 74; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or CC less and has a Koff rate constant of 1x10 power -3 s power -1 or CC less (both determined by surface plasmon resonance), and concurrentises human TNF-alpha cytotoxicity in a standard in vitro CC less (both determined by surface plasmon resonance), and continuous diseases, e.g. rheumatoicity in a standard in vitro CC inhibits TNF-alpha activity, can be used to treat sepsis, CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy mulltiple CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC burns, reperfusion injury, keloid formation, scar tissue formation, CC burns, reperfusion injury, keloid formation, scar tissue formation, CC burns, reperfusion molecule-1 (ELAM-1) on human umbilical vein CC endothelial cells (MUMPE)
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                                                                                                                                                                                                                                                                                                                  Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury;
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Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                       Homo sapiens.
W09729131-A1.
                                                                                                                                                                    bone resorption disease; coagulation disturbance; keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; pendotnelial disease; obesity; radiation molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W27591 standard; peptide; 12 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endothelial
                                                                                                                                              human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan umbilical vein endothelial cell.
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12 AA;
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                                                                                                                                              endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 27;
Pred. No. 2.39e+00;
2; Mismatches 0
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Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
WPI; 97-415302/38.

High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
Sclaim 20; Page 74; 102pp; English.

The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
C determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
cless and has a Koff rate constant of 1x10 power -3 s power -1 or
cless and has a Koff rate constant of 1x10 power -7 M or
cless tooth determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
cless (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
cless (both determined by surface plasmon resonance), and
neutralises numan TNF-alpha cytotoxicity in a standard in vitro
cless gondylitis, osteoarthritis, can be used to treat sepsis,
autoimmune diseases, e.g. Theumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
cardiac or inflammatory bone disorders, bone resorption disease,
clarkovite adhesion molycry, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
Ab also inhibits TNF-alpha induced expression of endothelial cell
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14-AUG-1997, U02219.
10-FEB-1997, U02219.
25-NOV-1996, US-031476.
09-FEB-1996, US-599226.
(BADI ) BASF AG.
                     Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                  Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton WPI; 97-415302/38.
                                                                                                                                                                                                                                                                                                                                                  keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BADI ) BASF AG
Allen DJ, Hooger
               The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W27590 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukocyte adhesion molecule-1 (ELAM-1) on human umbilical endothelial cells (HUVEC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells (HUVEC).
12 AA;
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US-599226.
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67; DB 27; Length 12
Pred. No. 3.06e+00;
1; Mismatches 1; Indels
                                                                                                     TNF alpha -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Labkovsky
                                                                               diseases
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                                                                                                   useful
                 complementarity
                                                                               and cancer
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Matches
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
                                                  autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease,
                                                                                                                                                                      The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complement determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 less and has a Koff rate constant of 1x10 power -3 s power -1 less (both determined by surface plasmon resonance), and neutralises human TNF-alpha (TNF-alpha activity, can be used to treat sepsis, inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid approximation of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the sepsis of the s
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High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 72; 102pp; English.
                         alcoholic, viral or fulminant hepatitis, coagulation disturbances,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukocyte adhesion endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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Pred. No. 6.36e+00;
2; Mismatches 1;
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formation,
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scar tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                         complementarity
                                                                                                                                                                                                                                                                                                                                 power -1 or
                                                                                                                                                                                                                                                                     in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
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                                                                                                             determining region 3 (CDR3).

C determining region 3 (CDR3).

C The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmo resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro cryotoxicity in a standard in vitro 1x92 assay with an ICS0 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple cardiac or inflammatory bone disorders, bone resorption disease, calcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
  Query Ma
Best Loc
Matches
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Best Local Similarity
Matches 9; Conser
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
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High affinity antibodies against human TNF alpha - useful to treat autoimmune diseases and claim 20; Page 73; 102pp; English.

TNF alpha settivity, e.g. to treat autoimmune diseases and claim 20; Page 73; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factors.
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W27589;
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endothelial cells (
Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
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W09729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease;
                                                                             Sequence
                                                                                                   endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell
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                      Local
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                        Similarity
                                                                               l cells (HUVEC).
12 AA;
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12 AA;
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81
                      . 88;
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Score 60; DB 27;
Pred. No. 1.66e+01;
2; Mismatches (
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Pred. No. 1.66e+01;
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                                                                                                                                                                                            RESULT
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BR WPI; 97-415302/38.

BR Albalso Inhibits DIF-Alpha autoimmune disease, obesity and radiation toxicity. The Ab ab also inhibits TWF-alpha induced expression of endothelial cell and the pain unballical wein.
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; bene resorption disease; coagulation toxicity; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
            Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; cardiac disorder; inflammatory bone disorder; reperfusion injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           л 9
w27587 standard; peptide; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                              endothelial cells (
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                                                                                                                                   19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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resorption disease; coagulation
                                                                                                                                                                                                                                                        ASYLSTASSLE 11
                                                                                                                                                                       standard;
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h JA, McGuiness BT, Roberts AJ, Sakorafas P,
JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                            . cells (HUVEC).
12 AA;
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                 80.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecule-1 (ELAM-1)
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                                                                                                                                                                                                                                                                                                                           Score 60; DB 27;
Pred. No. 1.66e+01;
2; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 on human umbilical vein
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The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro constant of 1x10 power -7 M or less. The Ab, which is sassy with an IC50 of 1x10 power -7 M or less. The Ab, which is inhibits TNF-alpha activity, can be used to tract sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, youty arthritis, allergy multiple syndrome, infectious diseases, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The hab also inhibits TNF-alpha induced expression of endothelial cell
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14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
10-FEB-1997;
25-NOV-1996;
09-FEB-1996;
                                                                                                                                        Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disease; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone tesorption disease; coagulation disturbance; burn; ELAM-1;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obseity; radiation toxicity;
                                                                                                                                                                                                                                                                                                               W27594 standard; peptide; W27594; 19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High affinity antibodies against human TNF alpha - useful i
TNF alpha activity, e.g. to treat autoimmune diseases and
Claim 9; Page 65; 102pp; English.
The present sequence is a novel anti-human tumour necrosis
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Allen DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                          Homo sapiens. 
WO9729131-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
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Salfeld JG, Schoenhaut D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-1996; US-
(BADI ) BASF AG.
                                                                                                                                endothelial cell leukocyte adhesion molecule-1
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                                                                                                                 human umbilical vein
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JA, McGuiness BT, Roberts AJ, Sakorafas P,
G, Schoenhaut D, Vaughan TJ, White M, Wilton
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 ; U02219.
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; US-599226.
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90.0%;
                                                                                                                 endothelial cell.
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Pred. No. 2.68e+01;
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PI High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PT slisclosure; Page 75; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1299 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, ostcoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CS syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
CC burns, reperfusion injury, kelold formation, scar tissue formation,
CC burns, reperfusion molecule-1 (ELAM-1) on human umbilical vein
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
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Best Local
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Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claim 14; Page 502; 1145pp; English.

This sequence is a H. pylori protein of unspecified function. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance
                                                                                                                                                                                                                                                                                                                        02-APR-1996;
25-OCT-1996;
28-OCT-1996;
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27-MAR-1997;
06-DEC-1996;
29-MAR-1996;
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Alm RA, Smith D;
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori ORF
Cytoplasmic; v
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Allen DJ
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WO9737044-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibitor; duodenal ulcer
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US-761318.
US-625811.
US-758731.
US-736905.
US-738859.
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A, McGuiness BT, Roberts AJ, Sakorafas
Schoenhaut D, Vaughan TJ, White M, Wi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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90.0%;
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Pred. No. 2.68e+01;
1; Mismatches 0
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                                                                                                                                                                                                                        The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC UnNand probes derived from it may be used for the identification of CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and CC can be used to prevent the translation of H. pylori mRNA. Antibodies capainst the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions cefined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR
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Matches
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Best Local :
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06-DEC-1996; US-761318.

29-MAR-1996; US-625811.

02-APR-1996; US-758731.

25-OCT-1996; US-736905.

28-OCT-1996; US-738859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. infection and for diagnosis of H. pylori infection Claims 14,80; Page 679; 1145pp; English. This sequence is a H. pylori cell envelope inner membrane pinvolved in cofactor metabolism.
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                                                                                                                                   Sequence
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Alm RA, Smith D;
WPI; 97-503122/46.
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76.0%;
llarity 80.0%;
Conservative
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                                                                                                                                                                                                recombinant polypeptide production,
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Score 57; DB 29;
Pred. No. 3.39e+01;
1; Mismatches 1
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Pred. No. 3.39e+01;
1; Mismatches 1
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                                                                                                                                                                                          1 H. pylori |
Lion, e.g. i
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Matches

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YLSTASSLEY 12

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RESULTY
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KW                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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CT The protein may be used in a vaccine to prevent or treat H. pylori confection or to identify H. pylori polypeptide binding compounds, consequence of the protein as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC acid sequences complementary to the DNA act as antisense sequences and cc can be used to prevent the translation of H. pylori mRNA. Antibodies can be used to prevent the translation of H. pylori mRNA. Antibodies can distribution of H. pylori-specific antigens. The genomic sequence of the pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions coding development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches
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06-DEC-1996; US-761318.

29-MAR-1996; US-625811.

02-APR-1996; US-758731.

25-OCT-1996; US-736905.

28-OCT-1996; US-738859.
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Alm RA, Smith D;
API; 97-503122/46.
N-PSDB; V25097.
Bankia gouldi endoglucanase. Endoglucanase; cellulose; bindoglucanase; cellulase; carboxymethylcellulose; cellulose; biomass; beta-1,4-glycosidic bond; hydrolysis; saccharification; thermostable enzyme; thermophilic; glycosidase. Bankia gouldi mix (Clone 37GP2). w09744361-A1.
                                                                                                                                                                                                                                                                                                                                                    LT 15
W34987 standard; Protein; 875
W34987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claims 14,80; Pages 947-948; 1145pp; English.

This sequence is a H. pylori cell envelope inner membrane protein the protein and the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein and pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane protein the pylori cell envelope inner membrane p
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||| ||:|||
3 YLSTASSLEY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 76.0%;
Local Similarity 80.0%;
ses 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB 29;
Pred. No. 3.39e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 526;
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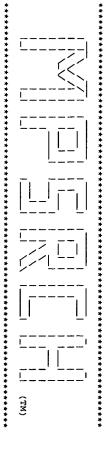
Search completed: Thu Sep Job time : 22 secs.

2 12:50:23 1999

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δÃ
                                      밁
                                                                                                                                                  Endoglucanase(s), preferably form archael bacterium, AEPII la-
y useful to degrade carboxymethylcellulose and hydrolyse of
peta-1,4-glycosidic bonds in cellulose
S Claim 1; Fig IC; 164pp; English.

This protein comprises an endoglucanase of Bankia gouldi mix (clone
37GP2) that is capable of degrading carboxymethylcellulose and of
hydrolyging the beta-1,4-glycosidic bonds in cellulose. It has
homology to an endoglucanase of archaebacterium AEPIIIa (see
W34985). It can be produced from native cells or from recombinant
host cells, especially prokaryotic host cells transformed with a
plasmid or virus-derived vector including the endoglucanase DNA
(see T94195). 24 Endoglucanases (see W34986-W35008) are claimed.
They can be used to degrade cellulose for the conversion of plant
biomass into fuels and chemicals, for use in detergents, textiles,
animal feed, waste treatment, and in the fruit juice and brewing
clindustries for the clarification and extraction of juices.
                                                                             Matches
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1997.
22-MAY-1997; U08793.
22-MAY-1996; US-651572.
(RECO-) RECOMBINANT BIOCATALYSIS INC.
Lam DE, Mathur EJ;
WPI; 98-018435/02.
N-PSDB; T94195.
                                  618 psyltvdsslty
                                                                         y Match 70.7%;
Local Similarity 58.3%;
hes 7; Conservative
  1 ASYLSTASSLEY 12
                                      629
                                                                         Score 53; DB 28;
Pred. No. 8.60e+01;
2; Mismatches 3
                                                                                                              Length 875;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 12:46:15 1999; MasPar time 3.60 Seconds
70.804 Million cell updates/sec

Sequence: 1 ASFLSTSSSLEY 12
Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-gengseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part14 15:part25 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part27 38:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.466; Variance 53.940; scale 0.324

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	Score	% Query Match	Length	₽B	Ħ	Description	Pred. No.
ב	74	100.0	12	27	W27592	Anti-TNF-alpha antibo	3.21e-01
N	69	93.2	12	27	W27588		1.19e+00
w	68	91.9	12	27	W27593	Anti-TNF-alpha antibo	1.54e+00
4	64	86.5	12	27	W27591	_	4.31e+00
5	63	85.1	121	27	W27569	_	5.56e+00
σ	61	82.4	12	27	W27590	_	9.22e+00
7	57	77.0	12	27	W27586	_	2.50e+01
8	57	77.0	12	27	W27589	Anti-TNF-alpha antibo	2.50e+01
9	57	77.0	12	27	W27587	_	2.50e+01
10	52	70.3	1026	17	R87146	Protocadherin clone 4	8.47e+01
11	52	70.3	1026	11	R58906	Human protocadherin-4	8.47e+01
12	52	70.3	1203	17	R87152	Alternatively spliced	8.47e+01
13	52	70.3	1203	11	R58911	Product of alternativ	8.47e+01
14	51	68.9	12	27	W27563	Anti-TNF-alpha antibo	1.08e+02
15	51	68.9	12	27	W27594	Anti-TNF-alpha antibo	1.08e+02
16	50	67.6	159	29	W55260	H. pylori ORF 06cp306	1.37e+02

45	44	43	42	41	40	39	38	37	36	3 5	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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7	N	9	ר	24	_	20	N	20	20	38	20	7	32	32	3	33	œ	21	38	21	14	28	37	15	12	29	17	29
Φ	*	7	w	W22613		W10066				633	8	799	504	503	503	504	395	681	981	18	301	498	022	46	291	568	54	47
equence of	Sequence of human col	CSF.	e of a	Human colony stimulat	cid s	long form CSF	SF derivati	a-3/C-delta-2	N-delta 3 LCSF.	injury asso	-3/c-	of human ma	a o	a pinoresino	a pinores	Į,	N-heparan sulphate su	omyces cerevi	coded by c	s cerevi	uivale	i er	succina.	cavenge	:omegalov	ori ORF 09cp1	ertussis toxin clon	ori ORF 06c
.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	4.38e+02	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	.38e+0	38	.38e+0	.38e+0	.48e+0	.48e+0	.48e+0	.48e+0	.76e+0	.19e	.19e+0	.73e	.73e+0	.37e+	.37e	.37e+

# ALIGNMENTS

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1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple		The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s nower -1 or	factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity	o; English.	High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer	WPI; 97-415302/38.	Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,	Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,		25-NOV-1996; US-031476.		14-AUG-1997.	WOQ779131-11	human umbilical vein endothelial cell.	endothelial cell leukocyte adhesion molecule-1;	<pre>neriodontal disease: chesity: radiation; pyrexia; HUVEC;</pre>	bone resorption disease; coagulation disturbance; burn; ELAM-1;	cardiac disorder; inflammatory bone disorder; reperfusion injury;	<pre>malignancy: pulmonary disorder: intestinal disorder: hepatitis:</pre>	heavy chain; complementarity determining region 3; inhibition;		o.	WZ/39Z; 19-MAR-1998 (first entry)	W27592 standard; peptide; 12 AA.	1

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                                                                                                                     determining region 3 (CDR3).

C determining region 3 (CDR3).

C determining region 3 (CDR3).

C The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmo resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which is inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial celling the procession of and the point of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition 
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiae disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; prexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothalial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; page 73; 102pp; English.
The present sequence is a novel anti-human tumour necrosi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mankovich JA, McGuiness B1
Salfeld JG, Schoenhaut D,
WPI; 97-415302/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1996;
09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-TNF-alpha antibody heavy chain CDR3. Human; tumour necrosis factor-alpha; TNF-alpha; heavy chain; complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9729131-A1.
                                                                                                        endothelial
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10-FEB-1997;
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; US-031476.
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No. 3.21e-01;
DB 27;
1.19e+00;
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3; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                necrosis
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Similarity

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Score Pred.

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Anti-TNF-alpha antibody heavy chain CDR3. Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                   High affinity antibodies against human TNF alpha - useful to inhibit profile activity, e.g. to treat autoimmune diseases and cancer SC claim 20; Page 75; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1292 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis.

Cautoinmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The ab also inhibits TNF-alpha induced expression of endothelial cell eleukoryte adhesion molecule-1 (FIAM-1) on human umbilical cell
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                               W27591 standard; peptide; W27591; 19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                        leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
Sequence 12 AA;
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salfeld JG, Schoenhaut D, WPI; 97-415302/38.
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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W27593;
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larity 83.3%;
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Pred. No. 1.54e+00;
2; Mismatches C
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factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
determining region 3 (CDR3).
The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
cupic assay with an IC50 of 1x10 power -7 M or less. The Ab, which
inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
scribac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, soar tissue formation,
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(BADI) BASF AG.

Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI: 97-415302/38.

HIGH affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 20; Page 74: 102pp; English.
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                                                                                                                                                                                                                                                                             malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                        keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                        treatment; sepsis; disease; autoimmune disease; infectious disease;
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Pred. No. 4.31e+00;
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Best Local
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                                                                                                                                                                                                                                                                                                                   malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                 High affinity antibodies against human TNF alpha activity, e.g. to treat autoi Claim 20; Page 74; 102pp; English.
                                                                                                           Mankovich JA, McGuiness BJ
Salfeld JG, Schoenhaut D,
WPI; 97-415302/38
                                                                                                                                                                                                      14-AUG-1997.
10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha;
heavy chain; complementarity determining region
treatment; sepsis; disease; autoimmune disease;
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Allen DJ, Hoogen
                                                                                                                                                                                                                                                                                Homo sapiens.
W09729131-A1.
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endothelial cells (HUVEC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mankovich JA,
                                   The present sequence is a novel anti-human tumour necrosis
                                                                                                                                                                    Allen DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High affinity antibodies against human
factor-alpha (TNF-alpha) antibody determining region 3 (CDR3).
                                                                                                                                                                                        (BADI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 sylstassldy 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 85.18;
Local Similarity 72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SFLSTSSSLEY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; peptide; 12
                                                                                                                                                                                        BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                         Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, JA, McGuiness BT, Roberts AJ, Sakorafas P, G, Schoenhaut D, Vaughan TJ, White M, Wilton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoogenboom HRJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells (HUVEC).
121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-599226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McGuiness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BT,
                                                                      to treat autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaymakcalan Z, Labkovs), Roberts AJ, Sakorafas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 63; DB 27; Length 12; Pred. No. 5.56e+00; 3; Mismatches 0; Indels
                 (AA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on human
                                                                                          TNF alpha -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF alpha - useful
               heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; CDR3
3; inhibition;
               complementarity
                                                                                          useful
                                                                      and
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                                                                        cancer
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                                                                                        to inhibit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                      autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diseases, autoimmune uveitis or nephrotic syndrome, infectious diseases, mallynancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease,
                                                                                                                                                                                                                                                                                                                                                                               10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-TNF-alpha antibody heavy chain CDR3.

Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                           Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         keloid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1; human umbilical vein endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
W09729131-A1.
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larity 75.0%;
Conservative
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             or fulminant hepatitis,
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             coagulation disturbances
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                                                                                                                                                                                                        The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid sepsis, autoimmune diseases, e.g. rheumatoid arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune weitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The burns inhibits TNF-alpha induced expression of endothelial cell
                                                                  Query Match
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Anti-TNF-alpha antibody heavy chain CDR3.
Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
Heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
cardiac disorder; arease: coaquiation disturbance; burn; ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wPI: 97-415302/38.

High affinity antibodies against human TNF alpha - TNF alpha activity, e.g. to treat autoimmune disea Claim 20; Page 73; 102pp; English.

The present sequence is a novel anti-human tumour factor-alpha (TNF-alpha) antibody (Ab) heavy chain determining region 3 (CDR3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W27589 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BADI ) BASF AG.
Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton
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endothelial cells (HUVEC).
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(BADI ) BASF AG.
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                                                                                                                                                              endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
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                                                                                                                                                                                           leukocyte adhesion molecule-1
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                                      Local
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      Similarity
9; Conser
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                                                                                                                                  12 AA;
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                                                                                                                                                           (HUVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUVEC).
                                      77.0%;
81.8%;
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81.8%;
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Score 57; D
Pred. No. 2.
2; Mismatcl
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Pred.
                                                                                                                                                                                        (ELAM-1)
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No. 2.50e+01;
                               DB 27;
2.50e+01;
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                                                                                                                                                                                        on human umbilical
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factor alpha (TNF alpha) antibody (Ab) heavy chain complementarity
determining region 3 (CD3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
yvrexia, periodontal disease, obesity and radiation toxicity. The
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
heavy chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
                                                                                                                         Protocadherin clone 42.
Protocadherin; pc3; pc4; pc5; human; catenin; therapy; clone; frog; fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer Claim 20; Page 73; 102pp; English.
                                                            WO9600289-A1.
                                                                                                                                                                                                                                                                                T 10
R87146 standard; Protein; 1026
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W09729131-A1.
                                04-JAN-1996.
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W27587 standard; peptide; 12
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12 AA;
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81.8%;
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Pred. No. 2.50e+01;
2; Mismatches 0
                                                                                                                             rat; cadherin; cell adhesion;
fly.
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                                                                                                                                                                     N-PSDB; Q68997.

N-PSDB; Q68997.

Polynucleotide sequences encoding new proto:cadherins - useful proto:cadherins - useful proto:cadherins - useful proto:cadherins - useful proto:cadherins - useful proto:cadherins - useful proto:cadherins - useful proto:cadherins - useful proto:cadherins - useful proto:cadherins - useful proto:cadherins of the human cDNAs corresp. to the partial cDNAs of two full length human cDNAs corresp. to the partial cDNAs of HUMAN-42 and HUMAN-43 (Q68981,Q68982) were isolated contained the putative entire coding sequences of two cDNAs which contained the putative entire coding sequences of two novel proteins designated protocadherin-42 (pc42) and protocadherin-43 (pc43). The DNA and deduced AA sequences of pc42 are in (pc43). The DNA and deduced AA sequences of pc42 are in (pc43). The DNA and deduced AA sequences of pc42 are in protocadherin such coverall structures of pc42 and pc43 are similar to that of typical cadherins but those of pc43 are similar to that of typical cadherins but they do have distinct features. Both lack the prosequences that are present in all known cadherin precursors. The extracellular domains of pc42 and pc43 are different in length conditions are contains seven subdomains that closely resemble the conditions. The sequences do not show any significant homology with those of known cadherins or cadherin-related proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities

Example 3; Page 71-75; 146pp; English.

This sequence represents a clone of the human protocadherin sequence, designated pc42. The cDNA encoding this sequence was isolated after screening a human foetal brain cDNA library (contained within lambdaZapII vectors), with 32P labelled versions of the sequences represented by r03605 and r03606. The cytoplasmic domain of cadherin interacts with the cytoskeleton through catenins and other cytoskeleton associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function.

The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. This protein sequence is involved in cell-cell adhesion. This sequence may have regulatory functions in the cell, as well as the cell-cell cused therapeutically.

Second of the component is a cytoplasmic domain appear to the component is involved in cell-cell adhesion. This sequence was functions in the cell, as well as the cell-cell cused therapeutically.
Query Match 70.3%;
Best Local Similarity 50.0%;
Matches 5; Conservative
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Best Local
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23-DEC-1993; U12588.
29-DEC-1992; US-998003
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R58906 standard; Protein; 1026
R58906;
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(DOHE-) DOHENY EYE INS'
SUZUKI S;
WPI; 96-068873/07.
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Local Similarity 50.0%;
nes 5; Conservative
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Score 52; DB 11;
Pred. No. 8.47e+01;
4; Mismatches 1
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Pred. No. 8.47e+01;
4; Mismatches 1
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CC This sequence represents a possible alternatively spliced version of the clone of the human protocadherin sequence, designated pc42. The cDNA cc encoding this sequence was isolated after screening a human foetal brain cCDNA library (contained within lambdaZapII vectors), with 32P labelled cc versions of the sequences represented by T03605 and T03601. The most cabundant spliced version of pc42 is represented in T03621. The cC cytoplasmic domain of cadherin interacts with the cytoskeleton through cc catenins and other cytoskeleton associated proteins. The cytoplasmic cdomain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different cethod from those with a cytoplasmic domain. This protein sequence is convolved in cell-cell adhesion. This sequence may have regulatory the contions in the cell, as well as the cell adhesive properties.

CC Antibodies produced against this sequence are useful for modulating the conditions of protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conse
                                                                                                                                                                                                                    momo sapiens.
W09414960-A.
07-JUL-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOHE-) Di
Suzuki S;
Polynucleotide sequences encoding new proto:cadherins - useful for modulating natural binding and regulating activities. Example: Page 84-89; 114pp; English.
Two full length human cDNAs corresp. to the partial cDNAs of HUMAN-42 and HUMAN-43 (068981,068982) were isolated from human fetal brain cDNA library. Several overlapping cDNA
                                                                                                                               Suzuki
WPI; 9
                                                                                                                                                                                                                                                                                                                                R58911
R58911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternatively spliced pc42.
Protocadherin; pc3; pc4; pc5; human; catenin; therapy; clone; frog; fruit
                                                                                                                                                                                 07-JUL-1994.
23-DEC-1993; U12588.
29-DEC-1992; US-998003
                                                                                                                                                                                                                                                                      Product of alternative splicing of human protocadherin-42 mRNA Cadherin; protocadherin; cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 96-068873/07.
N-PSDB; T03623.
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26-JUN-1995; U08071.
27-JUN-1994; US-268161.
                                                                                                               N-PSDB; Q68999
                                                                                                                                                                                                                                                                                                               17-APR-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                              standard; Protein; 1203
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                                                                                                                                                                  DOHENY EYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 1203
                                                                                                                                                                  INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 17;
Pred. No. 8.47e+01;
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C factor -alpha (TNF-alpha) antibody (Ab) heavy chain complementarity (determining region 3 (CDR3).

C The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or C less and has a Koff rate constant of 1x10 power -3 s power -1 or C less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro C 1292 assay with an IC50 of 1x10 power -7 M or less The Ab, which C inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, calcoholic, viral or fulminant hepatitis, coagulation disturbances,
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Best Local
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysis of various overlapping protocadherin cDNA clones revealed that some clones contd. unique sequences at the 3' end. The sequences forming the boundaries of the 3' end regions are consistent with the consensus sequence of mRNA splicing, suggesting that these clones may corresp. to alternatively spliced mRNAs. The DNA and AA sequences of one possible product of alternative splicing of pc42 mRNA are given in Q68999/R58911. The DNA and AA sequences of two possible products of alternative splicing of pc43 mRNA are respectively presented in Q69000/R58912 and Q69001/R49144. Sequence 1203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clones were isolated with each probe including two cDNAs which contained the putative entire coding sequences of two novel proteins designated protocadherin-42 (pc42) and protocadherin-43 (pc43). The DNA and deduced AA sequences of pc42 are in Q68997/R58906, while those of pc43 are in Q68998/R58907. Sequence
                                                                                                                                                                                                                                                                                                                                        High affinity antibodies against human TNF alpha - useful TNF alpha activity, e.g. to treat autoimmune diseases and Claim 9; Page 65; 102pp; English. The present sequence is a novel anti-human tumour necrosi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone resorption disease; coagulation disturbance; keloid formation; scar tissue formation; pyrexia; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Salfeld JG, Schoer WPI; 97-415302/38
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W27563 standard; peptide; 12 W27563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human umbilical vein endothelial cell.
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Similarity 50.0%;
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Pred. No. 8.47e+01;
4; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                               necrosis
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                                                                                                                                                                                                                                                                                                                                                                                           cancer
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pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).

Sequence 12 AA:

Query Match 68.9%; Best Local Similarity 70.0%; Matches 7; Conservative

Score 51; DB 27; Pred. No. 1.08e+02; Mismatches

Length 12

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                                                                                                                                                                                                                                  High activity, e.g. to treat autoimmune diseases and cancer PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer PS Disclosure; Page 75; 102p; English.

CT free present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CD3).

CT flee present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity determining region 3 (CD3).

CT flee Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less and has a Knoff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which cautismune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple CC syndrome, infectious diseases, autoimmune uveitis or nephrotic CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC cardiac or inflammatory bone disorders, bone resorption disease, CC syndrome, infectious diseases, malignancy, pulmonary, intestinal, CC alcoholic, viral or fulminant hepatitis, coagulation disturbances, CC burns, reperfusion injury, keloid formation, scar tissue formation, pyrevia, periodontal disease, obesity and radiation toxicity. The CC andothelial, cells (NITF-alpha induced expression of endothelial cell cendoryte adhesion molecule-1 (ELAM-1) on human umbilical vein
                                                                                                                  Query Match
Best Local S
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10-FEB-1997; U02219.
25-NOV-1996; US-031476.
09-FEB-1996; US-599226.
(BADI ) BASF AG.
Allen DJ, Hoogenboom HRJW, Kaymakcalan Z, Labkovsky B, Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.
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Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; heavy chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; benoid formation; scar tissue formation; pyrexia; HUVEC; periodontal disease; obesity; radiation toxicity; endothelial cell leukocyte adhesion molecule-1;
                                                                                                                                                                                                 endothelial cells (HUVEC).
Sequence 12 AA;
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                                                                                                                                                                                               Sequence
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2 SFLSTSSSLE 11
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larity 70.0%;
Conservative
                                                                                           Score 51; DB 27;
Pred. No. 1.08e+02;
3; Mismatches 0
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